GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 31, 2003, 13:55:32 ; Search time 83 Seconds
(without alignments)
128.129 Million cell updates/sec

Title: US-09-872-852-2
Perfect score: 367
Sequence: 1 MRIHYLLFALLFLFLVPVPG.....KEEQIGKCSTRGRKCCRRKK 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	367	100.0	67	20	AAY07244	Beta-defensin fami
2	367	100.0	67	21	AAB10602	Human SAP-3 pre-pr
3	367	100.0	67	23	AAO17768	Human beta-defensi
4	367	100.0	67	23	AAU91016	Transplant media a
5	367	100.0	67	23	AAU91036	Transplant media a
6	367	100.0	67	23	AAU09707	Human beta-defensi
7	357	97.3	65	20	AAY07243	Beta-defensin fami
8	250	68.1	45	21	AAB10600	Human SAP-3 mature
9	250	68.1	45	23	AAO17767	Human beta-defensi
10	250	68.1	45	23	AAU09709	Human beta-defensi
11	230	62.7	41	23	AAU09708	Human beta-defensi
12	225	61.3	40	23	AAO17766	Human beta-defensi
13	177	48.2	31	23	AAO17765	Human beta-defensi
14	177	48.2	31	23	AAM49572	Human beta-defensi
15	177	48.2	31	23	AAM49576	Human beta-defensi
16	173	47.1	32	21	AAB10621	Human SAP-3 N-term
17	163	44.4	51	20	AAY12039	Human 5' EST secre
18	148	40.3	27	23	AAO17773	Human beta-defensi
19	148	40.3	27	23	AAO17781	Human beta-defensi
20	136	37.1	24	23	AAO17774	Human beta-defensi
21	135	36.8	64	23	AAU91048	Transplant media a
22	133	36.2	64	20	AAW81071	Amino acid sequenc
23	133	36.2	64	23	AAU91049	Transplant media a
24	121.5	33.1	63	22	AAE02126	Mouse beta defensi
25	118	32.2	22	23	AAO17772	Human beta-defensi
26	113	30.8	64	17	AAR86894	Prepro-LAP. Bos t
27	113	30.8	64	23	AAU90965	Transplant media a
28	112	30.5	19	23	AAO17770	Human beta-defensi
29	111	30.2	64	13	AAR24332	Tracheal antimicro
30	111	30.2	64	16	AAR66205	Bovine tracheal an
31	111	30.2	64	16	AAR66204	Bovine tracheal an
32	111	30.2	64	19	AAW69696	Human tracheal ant
33	107.5	29.3	63	22	AAE02122	Mouse zamp3 (Defb5
34	107	29.2	65	17	AAR86896	Prepro-LAP #2. Sy
35	105	28.6	64	23	AAU91052	Transplant media a
36	100	27.2	64	23	AAU91051	Transplant media a
37	93	25.3	17	23	AAO17771	Human beta-defensi
38	93	25.3	17	23	AAO17780	Human beta-defensi
39	90.5	24.7	63	22	AAE02127	Mouse beta defensi
40	89	24.3	42	15	AAR63515	Bovine neutrophil
41	89	24.3	42	23	AAU91028	Transplant media a
42	85	23.2	69	19	AAW53857	Mouse beta defensi
43	85	23.2	69	22	AAE02125	Human zamp2 protei
44	78	21.3	80	22	AAB84568	Amino acid sequenc
45	76	20.7	80	22	AAB84567	Amino acid sequenc

ALIGNMENTS

RESULT 1
AAY07244
ID AAY07244 standard; Protein; 67 AA.
XX
AC AAY07244;
XX
DT 06-JUL-1999 (first entry)
XX
DE Beta-defensin family member zamp1.
XX
KW Human; zamp1; beta-defensin; bacterium; fungus; virus; inflammation;
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;
KW antibody; ion flux; cytocidal activity; mammalian cell.
XX
OS Homo sapiens.
XX
PN WO9913080-A1.
XX
PD 18-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US19222.
XX
PR 05-NOV-1997; 97US-0964687.
PR 10-SEP-1997; 97US-0058335.
PR 10-SEP-1997; 97US-0926529.
PR 05-NOV-1997; 97US-0064294.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Adler D, Baindur N, Beigel S, Holloway JL;
XX
DR WPI; 1999-215064/18.

DR N-PSDB; AAX29986.
XX
PT New zampl polypeptide and polynucleotide, human beta-defensins -
PT useful as diagnostic reagents and for treatment of microbial
PT infections, and AIDS
XX
PS Claim 1; Page 73; 79pp; English.
XX
CC This sequence represents the human zampl protein which is a member of the
CC beta-defensin protein family. Zampl protein is useful as a pharmaceutical
CC composition, useful for treatment of e.g. bacterial, fungal and viral
CC infections. They are also useful pro-inflammators, for treating chronic
CC tissue damage, and for stimulating the immune response, for treatment of
CC AIDS or chemotherapy patients. Zampl polypeptides and antibodies are
CC useful for studying activity of the melanocortin family, studying ion
CC flux in cell culture, and studying cytocidal activity against mammalian
CC cells in culture, by incubation with the cells. Zampl polypeptides are
CC especially useful for studying epithelial defensin induction in cell
CC culture when exposed to pathogenic stimuli.
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 367; DB 20; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
Db 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy 61 KCCRRKK 67
Db 61 KCCRRKK 67

RESULT 2
AAB10602
ID AAB10602 standard; Protein; 67 AA.
XX
AC AAB10602;
XX
DT 08-JAN-2001 (first entry)
XX
DE Human SAP-3 pre-protein.
XX
KW SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;
KW treatment; microbial infection; wound dressing; diagnostic reagent.
XX
OS Homo sapiens.
XX
PN WO200046245-A2.
XX
PD 10-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-EP00776.
XX
PR 01-FEB-1999; 99DE-1005128.
PR 08-OCT-1999; 99DE-1049436.
XX
PA (SCHD) SCHERING AG.
XX
PI Christophers E, Harder J, Schroeder J;
XX
DR WPI; 2000-514948/46.
DR N-PSDB; AAA71755.
XX
PT New human antibiotic peptides, useful for treating microbial
PT infections, particularly when incorporated in wound dressings, also
PT related nucleic acid -
XX
PS Claim 4; Page 39; 41pp; German.
XX
CC This invention describes the novel active, mature human proteins (I)
CC SAP-2 and SAP-3 which have antibiotic, antibacterial, antifungal and
CC antiviral activity. (I), and their precursors, are useful for treating
CC or preventing microbial infections (caused by bacteria, fungi or
CC viruses), particularly where they (or human cells expressing them) are
CC included in wound dressings, and to produce specific antibodies (Ab) or
CC their fragments. Ab are used as diagnostic reagents, e.g. to detect a
CC deficiency of (I) or the presence of a (I) variant. This sequence
CC represents the human SAP-3 protein described in the method of the
CC invention.
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 367; DB 21; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
Db 1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy 61 KCCRRKK 67
Db 61 KCCRRKK 67

RESULT 3
AAO17768
ID AAO17768 standard; protein; 67 AA.
XX
AC AAO17768;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human beta-defensin-3 derivative #3.
XX
KW Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
KW antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;
KW gastrointestinal tract; septicaemia; apoptosis induction; cancer.
XX
OS Homo sapiens.
XX
PN WO200240512-A2.
XX
PD 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-EP13174.
XX
PR 14-NOV-2000; 2000DE-1056365.
PR 30-MAR-2001; 2001DE-1016220.
XX
PA (IPFP-) IPF PHARM GMBH.
XX
PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;
PI Maegert H;
XX
DR WPI; 2002-435959/46.
XX
PT New human beta-defensin 3, useful for treating or preventing microbial
PT infection and tumors, also related nucleic acid -
XX
PS Claim 2; Page 23; 36pp; German.
XX
CC The present invention relates to human beta-defensin-3 (hBD-3) and its
CC derivatives. The peptide, its coding sequence and vectors containing the
CC coding sequence are useful in (gene) therapy and diagnosis, especially
CC for preventing or treating a wide range of microbial infections
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
CC respiratory tract, especially in cases of cystic fibrosis, and
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
CC and urogenital tracts, sepsis and yeast infections), and for inducing
CC apoptosis for treating malignant melanoma and tumours. The present
CC sequence is a derivative of human BD-3.

XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 367; DB 23; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67
```

RESULT 4
AAU91016
ID AAU91016 standard; Peptide; 67 AA.
XX
AC AAU91016;
XX
DT 05-JUN-2002 (first entry)
XX
DE Transplant media associated defensin peptide #17.
XX
KW Transplant; antimicrobial peptide; pore forming agent;
KW cell surface receptor binding compound; kidney transplant;
KW cardioplegia; organ transplant; transplant rejection; defensin.
XX
OS Homo sapiens.
XX
PN WO200209738-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US23785.
XX
PR 28-JUL-2000; 2000US-221632P.
PR 17-NOV-2000; 2000US-249602P.
PR 15-MAY-2001; 2001US-290932P.
XX
PA (MURP/) MURPHY C J.
XX
PI Murphy CJ, Reid TW, Mcanulty JF;
XX
DR WPI; 2002-268995/31.
XX
PT Media comprising antimicrobial polypeptides or pore forming agents
PT and/or cell surface receptor binding compounds useful for the storage
PT and preservation of organs prior to transplant -
XX
PS Claim 8; Page 28; 78pp; English.
XX
CC The invention describes new transplant compositions comprising
CC antimicrobial polypeptides or pore forming agents and/or cell surface
CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification)
CC alone. Lower serum creatinine levels are indicative of healthier kidneys
CC and a more preferable prognosis for the transplant patient. The media of
CC the invention are useful for decreasing the incidence and/or severity of
CC delayed graft function in patients receiving transplanted kidneys stored
CC and/or treated in the media. The media may also be used in procedures
CC such as cardioplegia. It is contemplated that transplant of healthier
CC organs leads to a decrease in chronic rejection. This sequence represents
CC an antimicrobial defensin peptide studied in the development of the
CC transplant media.
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 367; DB 23; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67
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RESULT 5
AAU91036
ID AAU91036 standard; Peptide; 67 AA.
XX
AC AAU91036;
XX
DT 05-JUN-2002 (first entry)
XX
DE Transplant media associated defensin peptide #37.
XX
KW Transplant; antimicrobial peptide; pore forming agent;
KW cell surface receptor binding compound; kidney transplant;
KW cardioplegia; organ transplant; transplant rejection; defensin.
XX
OS Homo sapiens.
XX
PN WO200209738-A1.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US23785.
XX
PR 28-JUL-2000; 2000US-221632P.
PR 17-NOV-2000; 2000US-249602P.
PR 15-MAY-2001; 2001US-290932P.
XX
PA (MURP/) MURPHY C J.
XX
PI Murphy CJ, Reid TW, Mcanulty JF;
XX
DR WPI; 2002-268995/31.
XX
PT Media comprising antimicrobial polypeptides or pore forming agents
PT and/or cell surface receptor binding compounds useful for the storage
PT and preservation of organs prior to transplant -
XX
PS Claim 8; Page 30; 78pp; English.
XX
CC The invention describes new transplant compositions comprising
CC antimicrobial polypeptides or pore forming agents and/or cell surface
CC receptor binding compounds. The media is capable of extending the
CC preservation period past 72 hours and can provide organs with increased
CC functionality upon transplant. animals receiving kidneys stored in the
CC media of the present invention for either three or four days had serum
CC creatinine levels of less than half of those observed in control animals
CC receiving kidneys stored in UW solution (defined in the specification)
CC alone. Lower serum creatinine levels are indicative of healthier kidneys
CC and a more preferable prognosis for the transplant patient. The media of
CC the invention are useful for decreasing the incidence and/or severity of
CC delayed graft function in patients receiving transplanted kidneys stored
CC and/or treated in the media. The media may also be used in procedures
CC such as cardioplegia. It is contemplated that transplant of healthier
CC organs leads to a decrease in chronic rejection. This sequence represents
CC an antimicrobial defensin peptide studied in the development of the
CC transplant media.
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 367; DB 23; Length 67;

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  Best Local Similarity   100.0%;  Pred. No. 1.5e-37;
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Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67
```

RESULT 6
AAU09707
ID AAU09707 standard; Protein; 67 AA.
XX
AC AAU09707;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human beta-defensin-3 (HBD-3).
XX
KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
KW microbial growth; microbial infection; pulmonary infection.
XX
OS Homo sapiens.
XX
PN WO200192309-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US18057.
XX
PR 01-JUN-2000; 2000US-208792P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI McCray PB, Tack B, Jia HP, Schutte BC;
XX
DR WPI; 2002-106302/14.
DR N-PSDB; AAS14407.
XX
PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,
PT useful for treating or preventing microbial growth or infection, or in
PT gene therapy -
XX
PS Claim 1; Page 96; 110pp; English.
XX
CC The present invention relates to the isolation of a novel antimicrobial
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of
CC inhibiting growth of a microbe by introducing into a host or environment
CC the antimicrobial peptide of the invention. The peptide is useful for
CC treating or preventing microbial growth or infections, e.g. pulmonary
CC infections when administered by inhalation. The peptide can be applied
CC on a work surface or a surgical instrument for the prevention and/or
CC suppression of microbial growth. The present sequence represents
CC HBD-3.
XX
SQ Sequence 67 AA;

```
  Query Match             100.0%;  Score 367;  DB 23;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-37;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
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Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67
```

RESULT 7
AAY07243
ID AAY07243 standard; Protein; 65 AA.
XX
AC AAY07243;
XX
DT 06-JUL-1999 (first entry)
XX
DE Beta-defensin family member zampl.
XX
KW Human; zampl; beta-defensin; bacterium; fungus; virus; inflammation;
KW tissue damage; immune response; AIDS; chemotherapy; melanocortin;
KW antibody; ion flux; cytocidal activity; mammalian cell.
XX
OS Homo sapiens.
XX
PN WO9913080-A1.
XX
PD 18-MAR-1999.
XX
PF 10-SEP-1998; 98WO-US19222.
XX
PR 05-NOV-1997; 97US-0964687.
PR 10-SEP-1997; 97US-0058335.
PR 10-SEP-1997; 97US-0926529.
PR 05-NOV-1997; 97US-0064294.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Adler D, Baindur N, Beigel S, Holloway JL;
XX
DR WPI; 1999-215064/18.
DR N-PSDB; AAX29985.
XX
PT New zampl polypeptide and polynucleotide, human beta-defensins -
PT useful as diagnostic reagents and for treatment of microbial
PT infections, and AIDS
XX
PS Claim 1; Page 70; 79pp; English.
XX
CC This sequence represents the human zampl protein which is a member of the
CC beta-defensin protein family. Zampl protein is useful as a pharmaceutical
CC composition, useful for treatment of e.g. bacterial, fungal and viral
CC infections. They are also useful pro-inflammators, for treating chronic
CC tissue damage, and for stimulating the immune response, for treatment of
CC AIDS or chemotherapy patients. Zampl polypeptides and antibodies are
CC useful for studying activity of the melanocortin family, studying ion
CC flux in cell culture, and studying cytocidal activity against mammalian
CC cells in culture, by incubation with the cells. Zampl polypeptides are
CC especially useful for studying epithelial defensin induction in cell
CC culture when exposed to pathogenic stimuli.
XX
SQ Sequence 65 AA;

```
  Query Match             97.3%;  Score 357;  DB 20;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-36;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
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Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRR 65
              |||||
Db         61 KCCRR 65
```

RESULT 8
AAB10600
ID AAB10600 standard; Protein; 45 AA.
XX
AC AAB10600;
XX

DT 08-JAN-2001 (first entry)
XX
DE Human SAP-3 mature protein.
XX
KW SAP-2; SAP-3; human; antibiotic; antibacterial; antifungal; antiviral;
KW treatment; microbial infection; wound dressing; diagnostic reagent.
XX
OS Homo sapiens.
XX
PN WO200046245-A2.
XX
PD 10-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-EP00776.
XX
PR 01-FEB-1999; 99DE-1005128.
PR 08-OCT-1999; 99DE-1049436.
XX
PA (SCHD) SCHERING AG.
XX
PI Christophers E, Harder J, Schroeder J;
XX
DR WPI; 2000-514948/46.
DR N-PSDB; AAA71753.
XX
PT New human antibiotic peptides, useful for treating microbial
PT infections, particularly when incorporated in wound dressings, also
PT related nucleic acid -
XX
PS Claim 1; Page 37; 41pp; German.
XX
CC This invention describes the novel active, mature human proteins (I)
CC SAP-2 and SAP-3 which have antibiotic, antibacterial, antifungal and
CC antiviral activity. (I), and their precursors, are useful for treating
CC or preventing microbial infections (caused by bacteria, fungi or
CC viruses), particularly where they (or human cells expressing them) are
CC included in wound dressings, and to produce specific antibodies (Ab) or
CC their fragments. Ab are used as diagnostic reagents, e.g. to detect a
CC deficiency of (I) or the presence of a (I) variant. This sequence
CC represents the mature human SAP-3 protein described in the method of the
CC invention.
XX
SQ Sequence 45 AA;

Query Match 68.1%; Score 250; DB 21; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
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Db 1 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 45

RESULT 9
AAO17767
ID AAO17767 standard; peptide; 45 AA.
XX
AC AAO17767;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human beta-defensin-3 derivative #2.
XX
KW Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
KW antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;
KW gastrointestinal tract; septicaemia; apoptosis induction; cancer.
XX
OS Homo sapiens.
XX
PN WO200240512-A2.
XX
PD 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-EP13174.
XX
PR 14-NOV-2000; 2000DE-1056365.
PR 30-MAR-2001; 2001DE-1016220.
XX
PA (IPFP-) IPF PHARM GMBH.
XX
PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;
PI Maegert H;
XX
DR WPI; 2002-435959/46.
XX
PT New human beta-defensin 3, useful for treating or preventing microbial
PT infection and tumors, also related nucleic acid -
XX
PS Claim 2; Page 23; 36pp; German.
XX
CC The present invention relates to human beta-defensin-3 (hBD-3) and its
CC derivatives. The peptide, its coding sequence and vectors containing the
CC coding sequence are useful in (gene) therapy and diagnosis, especially
CC for preventing or treating a wide range of microbial infections
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
CC respiratory tract, especially in cases of cystic fibrosis, and
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
CC and urogenital tracts, sepsis and yeast infections), and for inducing
CC apoptosis for treating malignant melanoma and tumours. The present
CC sequence is a derivative of human BD-3.
XX
SQ Sequence 45 AA;

Query Match 68.1%; Score 250; DB 23; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 45

RESULT 10
AAU09709
ID AAU09709 standard; Protein; 45 AA.
XX
AC AAU09709;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human beta-defensin-3 (HBD-3) mature protein sequence #2.
XX
KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
KW microbial growth; microbial infection; pulmonary infection.
XX
OS Homo sapiens.
XX
PN WO200192309-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US18057.
XX
PR 01-JUN-2000; 2000US-208792P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI McCray PB, Tack B, Jia HP, Schutte BC;
XX
DR WPI; 2002-106302/14.
XX
PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,
PT useful for treating or preventing microbial growth or infection, or in
PT gene therapy -
XX

PS Claim 29; Page 98; 110pp; English.
XX
CC The present invention relates to the isolation of a novel antimicrobial
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of
CC inhibiting growth of a microbe by introducing into a host or environment
CC the antimicrobial peptide of the invention. The peptide is useful for
CC treating or preventing microbial growth or infections, e.g. pulmonary
CC infections when administered by inhalation. The peptide can be applied
CC on a work surface or a surgical instrument for the prevention and/or
CC suppression of microbial growth. The present sequence represents
CC HBD-3 mature protein sequence #2.
XX
SQ Sequence 45 AA;

Query Match 68.1%; Score 250; DB 23; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
||||||||||||||||||||||||||||||||||||||||||||
Db 1 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 45

RESULT 11
AAU09708
ID AAU09708 standard; Protein; 41 AA.
XX
AC AAU09708;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human beta-defensin-3 (HBD-3) mature protein sequence #1.
XX
KW Human; antimicrobial peptide; human beta-defensin-3; HBD-3;
KW microbial growth; microbial infection; pulmonary infection.
XX
OS Homo sapiens.
XX
PN WO200192309-A2.
XX
PD 06-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-US18057.
XX
PR 01-JUN-2000; 2000US-208792P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI McCray PB, Tack B, Jia HP, Schutte BC;
XX
DR WPI; 2002-106302/14.
XX
PT New human beta-defensin 3 peptides and nucleic acids encoding peptides,
PT useful for treating or preventing microbial growth or infection, or in
PT gene therapy -
XX
PS Claim 28; Page 97; 110pp; English.
XX
CC The present invention relates to the isolation of a novel antimicrobial
CC peptide, human beta-defensin-3 (HBD-3). Also described is a method of
CC inhibiting growth of a microbe by introducing into a host or environment
CC the antimicrobial peptide of the invention. The peptide is useful for
CC treating or preventing microbial growth or infections, e.g. pulmonary
CC infections when administered by inhalation. The peptide can be applied
CC on a work surface or a surgical instrument for the prevention and/or
CC suppression of microbial growth. The present sequence represents
CC HBD-3 mature protein sequence #1.
XX
SQ Sequence 41 AA;

Query Match 62.7%; Score 230; DB 23; Length 41;
Best Local Similarity 100.0%; Pred. No. 6.1e-21;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
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Db 1 TLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 41

RESULT 12
AAO17766
ID AAO17766 standard; peptide; 40 AA.
XX
AC AAO17766;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human beta-defensin-3 derivative #1.
XX
KW Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
KW antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;
KW gastrointestinal tract; septicaemia; apoptosis induction; cancer.
XX
OS Homó sapiens.
XX
PN WO200240512-A2.
XX
PD 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-EP13174.
XX
PR 14-NOV-2000; 2000DE-1056365.
PR 30-MAR-2001; 2001DE-1016220.
XX
PA (IPFP-) IPF PHARM GMBH.
XX
PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;
PI Maegert H;
XX
DR WPI; 2002-435959/46.
XX
PT New human beta-defensin 3, useful for treating or preventing microbial
PT infection and tumors, also related nucleic acid -
XX
PS Claim 2; Page 23; 36pp; German.
XX
CC The present invention relates to human beta-defensin-3 (hBD-3) and its
CC derivatives. The peptide, its coding sequence and vectors containing the
CC coding sequence are useful in (gene) therapy and diagnosis, especially
CC for preventing or treating a wide range of microbial infections
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
CC respiratory tract, especially in cases of cystic fibrosis, and
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
CC and urogenital tracts, sepsis and yeast infections), and for inducing
CC apoptosis for treating malignant melanoma and tumours. The present
CC sequence is a derivative of human BD-3.
XX
SQ Sequence 40 AA;

Query Match 61.3%; Score 225; DB 23; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.4e-20;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
||||||||||||||||||||||||||||||||||||||||
Db 1 LQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 40

RESULT 13
AAO17765
ID AAO17765 standard; peptide; 31 AA.
XX
AC AAO17765;
XX
DT 30-AUG-2002 (first entry)

XX
DE Human beta-defensin-3.
XX
KW Human; beta-defensin-3; hBD-3; bacterial infection; gene therapy;
KW respiratory system; cystic fibrosis; inflammation; urogenital tract;
KW antibacterial; fungicide; cytostatic; antiinflammatory; antiulcer;
KW gastrointestinal tract; septicaemia; apoptosis induction; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "may be linked to between 1 and 50 amino acids"
FT Modified-site 31
FT /note= "may be linked to between 1 and 50 amino acids"
XX
PN WO200240512-A2.
XX
PD 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-EP13174.
XX
PR 14-NOV-2000; 2000DE-1056365.
PR 30-MAR-2001; 2001DE-1016220.
XX
PA (IPFP-) IPF PHARM GMBH.
XX
PI Forssmann W, Kluever E, Conejo-Garcia J, Adermann K, Bals R;
PI Maegert H;
XX
DR WPI; 2002-435959/46.
XX
PT New human beta-defensin 3, useful for treating or preventing microbial
PT infection and tumors, also related nucleic acid -
XX
PS Claim 1; Page 23; 36pp; German.
XX
CC The present invention relates to human beta-defensin-3 (hBD-3) and its
CC derivatives. The peptide, its coding sequence and vectors containing the
CC coding sequence are useful in (gene) therapy and diagnosis, especially
CC for preventing or treating a wide range of microbial infections
CC (particularly Burkholderia cepacia and Pseudomonas aeruginosa in the
CC respiratory tract, especially in cases of cystic fibrosis, and
CC Helicobacter pylori, also inflammatory diseases of the gastrointestinal
CC and urogenital tracts, sepsis and yeast infections), and for inducing
CC apoptosis for treating malignant melanoma and tumours. The present
CC sequence is human BD-3.
XX
SQ Sequence 31 AA;

Query Match 48.2%; Score 177; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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||||||||||||||||||||||||||||||
Db 1 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCC 31

RESULT 14
AAM49572
ID AAM49572 standard; peptide; 31 AA.
XX
AC AAM49572;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human beta-defensin hBD-5 peptide fragment #1.
XX
KW Defensin; human; antibacterial; antiinfertility; contraceptive;
KW peptide therapy; infection; gastrointestinal; respiratory tract;
KW urogenital tract; skin; gland; sperm penetration; systemic disease;
KW infertility; sperm inidation; sperm maturation; diagnostic marker;
KW inflammatory disease; epithelial organ; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200204487-A2.
XX
PD 17-JAN-2002.
XX
PF 11-JUL-2001; 2001WO-EP07973.
XX
PR 11-JUL-2000; 2000DE-1033505.
XX
PA (IPFP-) IPF PHARM GMBH.
XX
PI Forssmann W, Conejo-Garcia J, Adermann K;
XX
DR WPI; 2002-179697/23.
XX
PT New defensin type peptides useful for treatment of bacterial infections
PT and for fertility control, and as a diagnostic marker of inflammatory
PT disease in epithelial organs -
XX
PS Claim 2; Page 21; 41pp; German.
XX
CC This invention describes novel peptides (I) of the defensin type which
CC have antibacterial, antiinfertility and contraceptive activity and which
CC can be used for peptide therapy. (I), and their derivatives and
CC fragments, are used: (i) to treat bacterial infections, particularly of
CC the gastrointestinal, respiratory or urogenital tracts, or of the skin
CC and associated glands; (ii) to treat systemic diseases associated with
CC overexpression or deficiency of defensin production, particularly as
CC substitution therapy or by using (I)-specific antibodies; (iii) to treat
CC infertility, especially where the result of disordered sperm penetration,
CC inidation or maturation, also as contraceptives; and (iv) as a diagnostic
CC marker of inflammatory disease in epithelial organs. Both chronic and
CC acute diseases may be treated, e.g. in intensive care. Also genes that
CC encode (I) can be used for systemic or localised gene therapy of the
CC specified diseases, in epithelial tissues or organs. (I) have exceptional
CC biological activity and since they do not induce an immune response, they
CC are particularly well suited for long-term use. This sequence represents
CC a human defensin described in the disclosure of the invention.
XX
SQ Sequence 31 AA;

Query Match 48.2%; Score 177; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCC 63
||||||||||||||||||||||||||||||
Db 1 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCC 31

RESULT 15
AAM49576
ID AAM49576 standard; peptide; 31 AA.
XX
AC AAM49576;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human beta-defensin hBD-6 peptide fragment #2.
XX
KW Defensin; human; antibacterial; antiinfertility; contraceptive;
KW peptide therapy; infection; gastrointestinal; respiratory tract;
KW urogenital tract; skin; gland; sperm penetration; systemic disease;
KW infertility; sperm inidation; sperm maturation; diagnostic marker;
KW inflammatory disease; epithelial organ; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200204487-A2.
XX

PD 17-JAN-2002.
XX
PF 11-JUL-2001; 2001WO-EP07973.
XX
PR 11-JUL-2000; 2000DE-1033505.
XX
PA (IPFP-) IPF PHARM GMBH.
XX
PI Forssmann W, Conejo-Garcia J, Adermann K;
XX
DR WPI; 2002-179697/23.
XX
PT New defensin type peptides useful for treatment of bacterial infections
PT and for fertility control, and as a diagnostic marker of inflammatory
PT disease in epithelial organs -
XX
PS Claim 3; Page 22; 41pp; German.
XX
CC This invention describes novel peptides (I) of the defensin type which
CC have antibacterial, antiinfertility and contraceptive activity and which
CC can be used for peptide therapy. (I), and their derivatives and
CC fragments, are used: (i) to treat bacterial infections, particularly of
CC the gastrointestinal, respiratory or urogenital tracts, or of the skin
CC and associated glands; (ii) to treat systemic diseases associated with
CC overexpression or deficiency of defensin production, particularly as
CC substitution therapy or by using (I)-specific antibodies; (iii) to treat
CC infertility, especially where the result of disordered sperm penetration,
CC inidation or maturation, also as contraceptives; and (iv) as a diagnostic
CC marker of inflammatory disease in epithelial organs. Both chronic and
CC acute diseases may be treated, e.g. in intensive care. Also genes that
CC encode (I) can be used for systemic or localised gene therapy of the
CC specified diseases, in epithelial tissues or organs. (I) have exceptional
CC biological activity and since they do not induce an immune response, they
CC are particularly well suited for long-term use. This sequence represents
CC a human defensin described in the disclosure of the invention.
XX
SQ Sequence 31 AA;

Query Match 48.2%; Score 177; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCC 63
              |||||||||||||||||||||||||||||||
Db          1 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCC 31
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Search completed: October 31, 2003, 14:01:30
Job time : 84 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 31, 2003, 14:01:37 ; Search time 29 Seconds
(without alignments)
97.753 Million cell updates/sec

Title: US-09-872-852-2
Perfect score: 367
Sequence: 1 MRIHYLLFALLFLFLVPVPG.....KEEQIGKCSTRGRKCCRRKK 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	367	100.0	67	4	US-09-868-659-4	Sequence 4, Appli
2	367	100.0	67	4	US-09-636-399A-10	Sequence 10, Appl
3	357	97.3	65	4	US-09-636-399A-2	Sequence 2, Appli
4	250	68.1	45	4	US-09-868-659-2	Sequence 2, Appli
5	241	65.7	49	4	US-09-636-399A-35	Sequence 35, Appl
6	236	64.3	48	4	US-09-636-399A-36	Sequence 36, Appl
7	234	63.8	48	4	US-09-636-399A-37	Sequence 37, Appl
8	229	62.4	47	4	US-09-636-399A-38	Sequence 38, Appl
9	228	62.1	47	4	US-09-636-399A-39	Sequence 39, Appl
10	223	60.8	46	4	US-09-636-399A-40	Sequence 40, Appl
11	220	59.9	46	4	US-09-636-399A-41	Sequence 41, Appl
12	215	58.6	45	4	US-09-636-399A-42	Sequence 42, Appl
13	214	58.3	45	4	US-09-636-399A-43	Sequence 43, Appl
14	209	56.9	44	4	US-09-636-399A-44	Sequence 44, Appl
15	208	56.7	44	4	US-09-636-399A-20	Sequence 20, Appl
16	208	56.7	44	4	US-09-636-399A-45	Sequence 45, Appl
17	204	55.6	43	4	US-09-636-399A-23	Sequence 23, Appl
18	204	55.6	43	4	US-09-636-399A-47	Sequence 47, Appl
19	203	55.3	43	4	US-09-636-399A-21	Sequence 21, Appl
20	203	55.3	43	4	US-09-636-399A-46	Sequence 46, Appl
21	200	54.5	42	4	US-09-636-399A-26	Sequence 26, Appl
22	200	54.5	42	4	US-09-636-399A-49	Sequence 49, Appl
23	199	54.2	42	4	US-09-636-399A-24	Sequence 24, Appl
24	199	54.2	42	4	US-09-636-399A-48	Sequence 48, Appl
25	198	54.0	42	4	US-09-636-399A-22	Sequence 22, Appl
26	195	53.1	41	4	US-09-636-399A-27	Sequence 27, Appl
27	195	53.1	41	4	US-09-636-399A-50	Sequence 50, Appl
28	194	52.9	41	4	US-09-636-399A-25	Sequence 25, Appl
29	194	52.9	41	4	US-09-636-399A-29	Sequence 29, Appl
30	194	52.9	41	4	US-09-636-399A-51	Sequence 51, Appl
31	190	51.8	40	4	US-09-636-399A-28	Sequence 28, Appl
32	189	51.5	40	4	US-09-636-399A-30	Sequence 30, Appl
33	189	51.5	40	4	US-09-636-399A-32	Sequence 32, Appl
34	189	51.5	40	4	US-09-636-399A-52	Sequence 52, Appl
35	189	51.5	40	4	US-09-636-399A-53	Sequence 53, Appl
36	185	50.4	39	4	US-09-636-399A-19	Sequence 19, Appl
37	185	50.4	39	4	US-09-636-399A-55	Sequence 55, Appl
38	184	50.1	39	4	US-09-636-399A-31	Sequence 31, Appl
39	184	50.1	39	4	US-09-636-399A-33	Sequence 33, Appl
40	184	50.1	39	4	US-09-636-399A-54	Sequence 54, Appl
41	182	49.6	37	4	US-09-636-399A-59	Sequence 59, Appl
42	182	49.6	38	4	US-09-636-399A-57	Sequence 57, Appl
43	180	49.0	38	4	US-09-636-399A-18	Sequence 18, Appl
44	180	49.0	38	4	US-09-636-399A-56	Sequence 56, Appl
45	179	48.8	38	4	US-09-636-399A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-868-659-4
; Sequence 4, Application US/09868659
; Patent No. 6568002
; GENERAL INFORMATION:
; APPLICANT: CHRISTOPHERS, ENNO
; APPLICANT: HARDER, JURGEN
; APPLICANT: SCHRODER, JENS
; TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS
; FILE REFERENCE: SCH-1813A
; CURRENT APPLICATION NUMBER: US/09/868,659
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: PCT/EP00/00776
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: DE 199 05 128.9
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: DE 199 49 436.3
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-868-659-4

Query Match 100.0%; Score 367; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 KCCRRKK 67
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Db         61 KCCRRKK 67
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RESULT 2
US-09-636-399A-10
; Sequence 10, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS

; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-10

Query Match 100.0%; Score 367; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 2e-38;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67
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RESULT 3
US-09-636-399A-2
; Sequence 2, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-2

Query Match 97.3%; Score 357; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 3.3e-37;
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRR 65
              |||||
Db         61 KCCRR 65
```

RESULT 4
US-09-868-659-2
; Sequence 2, Application US/09868659
; Patent No. 6568002
; GENERAL INFORMATION:
; APPLICANT: CHRISTOPHERS, ENNO
; APPLICANT: HARDER, JURGEN
; APPLICANT: SCHRODER, JENS
; TITLE OF INVENTION: HUMAN ANTIBIOTIC PROTEINS
; FILE REFERENCE: SCH-1813A
; CURRENT APPLICATION NUMBER: US/09/868,659
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: PCT/EP00/00776
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: DE 199 05 128.9
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: DE 199 49 436.3
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-868-659-2

Query Match 68.1%; Score 250; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.9e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         23 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 45
```

RESULT 5
US-09-636-399A-35
; Sequence 35, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-35

Query Match 65.7%; Score 241; DB 4; Length 49;

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  Best Local Similarity   91.8%;  Pred. No. 5.6e-23;
  Matches   45;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         19 PGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 PGHGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 49


RESULT 6
US-09-636-399A-36
; Sequence 36, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
;  CURRENT APPLICATION NUMBER: US/09/636,399A
;  CURRENT FILING DATE:  2000-08-10
;  PRIOR APPLICATION NUMBER: 60/058,335
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
;   LENGTH: 48
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Defensin polypeptide
;   NAME/KEY: VARIANT
;   LOCATION: (45)...(45)
;   OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-36

  Query Match             64.3%;  Score 236;  DB 4;  Length 48;
  Best Local Similarity   91.7%;  Pred. No. 2.3e-22;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         19 PGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRK 66
              |||||||||||| |||||||||||||||||||| ||| ||||||| |||
Db          1 PGHGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRK 48


RESULT 7
US-09-636-399A-37
; Sequence 37, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
;  CURRENT APPLICATION NUMBER: US/09/636,399A
;  CURRENT FILING DATE:  2000-08-10
;  PRIOR APPLICATION NUMBER: 60/058,335
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
;   LENGTH: 48
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Defensin polypeptide
;   NAME/KEY: VARIANT
;   LOCATION: (44)...(44)
;   OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-37

  Query Match             63.8%;  Score 234;  DB 4;  Length 48;
  Best Local Similarity   91.7%;  Pred. No. 4e-22;
  Matches   44;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         20 GHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 GHGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 48


RESULT 8
US-09-636-399A-38
; Sequence 38, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
;  CURRENT APPLICATION NUMBER: US/09/636,399A
;  CURRENT FILING DATE:  2000-08-10
;  PRIOR APPLICATION NUMBER: 60/058,335
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
;   LENGTH: 47
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Defensin polypeptide
;   NAME/KEY: VARIANT
;   LOCATION: (44)...(44)
;   OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met.
US-09-636-399A-38

  Query Match             62.4%;  Score 229;  DB 4;  Length 47;
  Best Local Similarity   91.5%;  Pred. No. 1.6e-21;
  Matches   43;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         20 GHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRK 66
              |||||||||| |||||||||||||||||||| ||| ||||||| |||
Db          1 GHGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRK 47


RESULT 9
US-09-636-399A-39
; Sequence 39, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
```

; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (43)...(43)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-09-636-399A-39

Query Match 62.1%; Score 228; DB 4; Length 47;
Best Local Similarity 91.5%; Pred. No. 2.2e-21;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         21 HGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              ||||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 HGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 47
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RESULT 10
US-09-636-399A-40
; Sequence 40, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (43)...(43)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-40

Query Match 60.8%; Score 223; DB 4; Length 46;
Best Local Similarity 91.3%; Pred. No. 8.9e-21;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         21 HGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRK 66
              ||||||||| |||||||||||||||||||| ||| ||||||| |||
Db          1 HGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRK 46
```

RESULT 11
US-09-636-399A-41
; Sequence 41, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (42)...(42)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-41

Query Match 59.9%; Score 220; DB 4; Length 46;
Best Local Similarity 91.3%; Pred. No. 2.1e-20;
Matches 42; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         22 GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 GGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 46
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RESULT 12
US-09-636-399A-42
; Sequence 42, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAMB/KEY: VARIANT
; LOCATION: (42)...(42)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-42

Query Match 58.6%; Score 215; DB 4; Length 45;
Best Local Similarity 91.1%; Pred. No. 8.5e-20;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         22 GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRK 66
              |||||||| |||||||||||||||||||| ||| ||||||| |||
Db          1 GGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRK 45
```

RESULT 13
US-09-636-399A-43
; Sequence 43, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAMB/KEY: VARIANT
; LOCATION: (41)...(41)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-43

Query Match 58.3%; Score 214; DB 4; Length 45;
Best Local Similarity 91.1%; Pred. No. 1.1e-19;
Matches 41; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         23 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              ||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 GIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 45
```

RESULT 14
US-09-636-399A-44
; Sequence 44, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; NAME/KEY: VARIANT
; LOCATION: (41)...(41)
; OTHER INFORMATION: Xaa is Leu, Ile, Phe, Val, or Met
US-09-636-399A-44

Query Match 56.9%; Score 209; DB 4; Length 44;
Best Local Similarity 90.9%; Pred. No. 4.6e-19;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         23 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRK 66
              ||||||| |||||||||||||||||||| ||| ||||||| |||
Db          1 GIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRK 44
```

RESULT 15
US-09-636-399A-20
; Sequence 20, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin Polypeptide
US-09-636-399A-20

Query Match 56.7%; Score 208; DB 4; Length 44;
Best Local Similarity 90.9%; Pred. No. 6.1e-19;

Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         24 IINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              ||||||||||||  |||||||||||||| ||||| |||||||
Db          1 IINTLQKYYCRVRYYRCAVLSCLPKEEQIYKCSTRYRKCCRRKK 44
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Job time : 29 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 31, 2003, 14:00:07 ; Search time 28 Seconds
(without alignments)
409.528 Million cell updates/sec

Title: US-09-872-852-2
Perfect score: 367
Sequence: 1 MRIHYLLFALLFLFLVPVPG.....KEEQIGKCSTRGRKCCRRKK 67

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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	367	100.0	67	9	US-09-917-340-52	Sequence 52, Appl
2	367	100.0	67	9	US-09-917-340-72	Sequence 72, Appl
3	367	100.0	67	10	US-09-872-852-2	Sequence 2, Appli
4	367	100.0	67	12	US-10-091-166B-10	Sequence 10, Appl
5	367	100.0	67	12	US-10-272-121-10	Sequence 10, Appl
6	367	100.0	67	12	US-10-409-366-10	Sequence 10, Appl
7	367	100.0	67	12	US-10-409-532-10	Sequence 10, Appl
8	357	97.3	65	12	US-10-091-166B-2	Sequence 2, Appli
9	357	97.3	65	12	US-10-272-121-2	Sequence 2, Appli
10	357	97.3	65	12	US-10-409-366-2	Sequence 2, Appli
11	357	97.3	65	12	US-10-409-532-2	Sequence 2, Appli
12	250	68.1	45	10	US-09-872-852-4	Sequence 4, Appli
13	241	65.7	49	12	US-10-091-166B-35	Sequence 35, Appl
14	241	65.7	49	12	US-10-272-121-35	Sequence 35, Appl
15	241	65.7	49	12	US-10-409-366-35	Sequence 35, Appl
16	241	65.7	49	12	US-10-409-532-35	Sequence 35, Appl
17	236	64.3	48	12	US-10-091-166B-36	Sequence 36, Appl
18	236	64.3	48	12	US-10-272-121-36	Sequence 36, Appl
19	236	64.3	48	12	US-10-409-366-36	Sequence 36, Appl
20	236	64.3	48	12	US-10-409-532-36	Sequence 36, Appl
21	234	63.8	48	12	US-10-091-166B-37	Sequence 37, Appl
22	234	63.8	48	12	US-10-272-121-37	Sequence 37, Appl
23	234	63.8	48	12	US-10-409-366-37	Sequence 37, Appl
24	234	63.8	48	12	US-10-409-532-37	Sequence 37, Appl
25	230	62.7	41	10	US-09-872-852-3	Sequence 3, Appli
26	229	62.4	47	12	US-10-091-166B-38	Sequence 38, Appl
27	229	62.4	47	12	US-10-272-121-38	Sequence 38, Appl
28	229	62.4	47	12	US-10-409-366-38	Sequence 38, Appl
29	229	62.4	47	12	US-10-409-532-38	Sequence 38, Appl
30	228	62.1	47	12	US-10-091-166B-39	Sequence 39, Appl
31	228	62.1	47	12	US-10-272-121-39	Sequence 39, Appl
32	228	62.1	47	12	US-10-409-366-39	Sequence 39, Appl
33	228	62.1	47	12	US-10-409-532-39	Sequence 39, Appl
34	223	60.8	46	12	US-10-091-166B-40	Sequence 40, Appl
35	223	60.8	46	12	US-10-272-121-40	Sequence 40, Appl
36	223	60.8	46	12	US-10-409-366-40	Sequence 40, Appl
37	223	60.8	46	12	US-10-409-532-40	Sequence 40, Appl
38	220	59.9	46	12	US-10-091-166B-41	Sequence 41, Appl
39	220	59.9	46	12	US-10-272-121-41	Sequence 41, Appl
40	220	59.9	46	12	US-10-409-366-41	Sequence 41, Appl
41	220	59.9	46	12	US-10-409-532-41	Sequence 41, Appl
42	215	58.6	45	12	US-10-091-166B-42	Sequence 42, Appl
43	215	58.6	45	12	US-10-272-121-42	Sequence 42, Appl
44	215	58.6	45	12	US-10-409-366-42	Sequence 42, Appl
45	215	58.6	45	12	US-10-409-532-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-917-340-52
; Sequence 52, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-340-52

Query Match 100.0%; Score 367; DB 9; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67
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RESULT 2
US-09-917-340-72
; Sequence 72, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Christopher J.
;  APPLICANT:  McAnulty, Jonathan F.
;  APPLICANT:  Reid, Ted W.
;  TITLE OF INVENTION: Transplant Media
;  FILE REFERENCE: TPLANT-06468
;  CURRENT APPLICATION NUMBER: US/09/917,340
;  CURRENT FILING DATE:  2001-07-29
;  PRIOR APPLICATION NUMBER: 60/221,632
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 60/249,602
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/290,932
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-917-340-72

  Query Match           100.0%;  Score 367;  DB 9;  Length 67;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-37;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67


RESULT 3
US-09-872-852-2
; Sequence 2, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
;  APPLICANT: MCCRAY JR, PAUL B.
;  APPLICANT:  TACK, BRIAN
;  APPLICANT:  JIA, HONG PENG
;  APPLICANT:  SCHUTTE, BRIAN C.
;  TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
;  TITLE OF INVENTION:  BETA-DEFENSIN ANTIMICROBIAL PEPTIDE
;  FILE REFERENCE: IOWA:031US
;  CURRENT APPLICATION NUMBER: US/09/872,852
;  CURRENT FILING DATE:  2001-06-01
;  PRIOR APPLICATION NUMBER: 60/208,792
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-09-872-852-2

  Query Match           100.0%;  Score 367;  DB 10;  Length 67;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-37;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67


RESULT 4
US-10-091-166B-10
; Sequence 10, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44D1
;  CURRENT APPLICATION NUMBER: US/10/091,166B
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: US 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 09/344,097
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/058,335
;  PRIOR FILING DATE: 1997-09-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-091-166B-10

  Query Match           100.0%;  Score 367;  DB 12;  Length 67;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-37;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67


RESULT 5
US-10-272-121-10
; Sequence 10, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44D2
;  CURRENT APPLICATION NUMBER: US/10/272,121
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: US 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 09/344,097
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/064,294
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;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/058,335
;  PRIOR FILING DATE: 1997-09-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-272-121-10

  Query Match             100.0%;  Score 367;  DB 12;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-37;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67


RESULT 6
US-10-409-366-10
; Sequence 10, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
;  CURRENT APPLICATION NUMBER: US/10/409,366
;  CURRENT FILING DATE:  2003-04-07
;  PRIOR APPLICATION NUMBER: US/09/636,399A
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: 60/058,335
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-409-366-10

  Query Match             100.0%;  Score 367;  DB 12;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-37;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67


RESULT 7
US-10-409-532-10
; Sequence 10, Application US/10409532
; Publication No. US20030166913A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
;  CURRENT APPLICATION NUMBER: US/10/409,532
;  CURRENT FILING DATE:  2003-04-07
;  PRIOR APPLICATION NUMBER: US/09/636,399A
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: 60/058,335
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-409-532-10

  Query Match             100.0%;  Score 367;  DB 12;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-37;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67


RESULT 8
US-10-091-166B-2
; Sequence 2, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44D1
;  CURRENT APPLICATION NUMBER: US/10/091,166B
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: US 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 09/344,097
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/058,335
;  PRIOR FILING DATE: 1997-09-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-091-166B-2
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  Query Match             97.3%;  Score 357;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-36;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRR 65
              |||||
Db         61 KCCRR 65


RESULT 9
US-10-272-121-2
; Sequence 2, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44D2
;  CURRENT APPLICATION NUMBER: US/10/272,121
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: US 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 09/344,097
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/058,335
;  PRIOR FILING DATE: 1997-09-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-272-121-2

  Query Match             97.3%;  Score 357;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-36;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRR 65
              |||||
Db         61 KCCRR 65


RESULT 10
US-10-409-366-2
; Sequence 2, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
;  CURRENT APPLICATION NUMBER: US/10/409,366
;  CURRENT FILING DATE:  2003-04-07
;  PRIOR APPLICATION NUMBER: US/09/636,399A
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: 60/058,335
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-409-366-2

  Query Match             97.3%;  Score 357;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-36;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRR 65
              |||||
Db         61 KCCRR 65


RESULT 11
US-10-409-532-2
; Sequence 2, Application US/10409532
; Publication No. US20030166913A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
;  CURRENT APPLICATION NUMBER: US/10/409,532
;  CURRENT FILING DATE:  2003-04-07
;  PRIOR APPLICATION NUMBER: US/09/636,399A
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: 60/058,335
;  PRIOR FILING DATE: 1997-10-09
;  PRIOR APPLICATION NUMBER: 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 65
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-409-532-2

  Query Match             97.3%;  Score 357;  DB 12;  Length 65;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-36;
  Matches   65;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRR 65
              |||||
Db         61 KCCRR 65
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RESULT 12
US-09-872-852-4
; Sequence 4, Application US/09872852
; Patent No. US20020115602A1
; GENERAL INFORMATION:
;  APPLICANT: MCCRAY JR, PAUL B.
;  APPLICANT:  TACK, BRIAN
;  APPLICANT:  JIA, HONG PENG
;  APPLICANT:  SCHUTTE, BRIAN C.
;  TITLE OF INVENTION: HUMAN BETA-DEFENSIN-3 (HBD-3), A HIGHLY CATIONIC
;  TITLE OF INVENTION:  BETA-DEFENSIN ANTIMICROBIAL PEPTIDE
;  FILE REFERENCE: IOWA:031US
;  CURRENT APPLICATION NUMBER: US/09/872,852
;  CURRENT FILING DATE:  2001-06-01
;  PRIOR APPLICATION NUMBER: 60/208,792
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Synthetic
;   OTHER INFORMATION: Peptide
US-09-872-852-4

  Query Match             68.1%;  Score 250;  DB 10;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-23;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         23 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 45


RESULT 13
US-10-091-166B-35
; Sequence 35, Application US/10091166B
; Publication No. US20030143671A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44D1
;  CURRENT APPLICATION NUMBER: US/10/091,166B
;  CURRENT FILING DATE:  2002-03-05
;  PRIOR APPLICATION NUMBER: US 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 09/344,097
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/058,335
;  PRIOR FILING DATE: 1997-09-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 49
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Defensin polypeptide
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (45)...(45)
;   OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
;   OTHER INFORMATION: methionine
US-10-091-166B-35

  Query Match             65.7%;  Score 241;  DB 12;  Length 49;
  Best Local Similarity   91.8%;  Pred. No. 3.3e-22;
  Matches   45;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         19 PGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 PGHGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 49


RESULT 14
US-10-272-121-35
; Sequence 35, Application US/10272121
; Publication No. US20030157638A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44D2
;  CURRENT APPLICATION NUMBER: US/10/272,121
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: US 09/636,399
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US 09/344,097
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: US 09/150,786
;  PRIOR FILING DATE: 1998-09-10
;  PRIOR APPLICATION NUMBER: US 60/064,294
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/058,335
;  PRIOR FILING DATE: 1997-09-10
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
;   LENGTH: 49
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Defensin polypeptide
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (45)...(45)
;   OTHER INFORMATION: leucine, isoleucine, valine, phenylalanine, or
;   OTHER INFORMATION: methionine
US-10-272-121-35

  Query Match             65.7%;  Score 241;  DB 12;  Length 49;
  Best Local Similarity   91.8%;  Pred. No. 3.3e-22;
  Matches   45;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         19 PGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 PGHGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 49


RESULT 15
US-10-409-366-35
; Sequence 35, Application US/10409366
; Publication No. US20030166912A1
; GENERAL INFORMATION:
;  APPLICANT: Adler, David A.
;  APPLICANT:  Holloway, James L.
;  APPLICANT:  Baindur, Nand
;  APPLICANT:  Beigel-Orme, Stephanie
;  APPLICANT:  Sheppard, Paul O.
;  TITLE OF INVENTION: NOVEL BETA-DEFENSINS
;  FILE REFERENCE: 97-44C2
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; CURRENT APPLICATION NUMBER: US/10/409,366
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/636,399A
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Defensin polypeptide
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (45)...(45)
; OTHER INFORMATION: Xaa is Leu, Ile, Val, Phe, or Met
US-10-409-366-35

Query Match 65.7%; Score 241; DB 12; Length 49;
Best Local Similarity 91.8%; Pred. No. 3.3e-22;
Matches 45; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy         19 PGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKK 67
              |||||||||| |||||||||||||||||||| ||| ||||||| ||||
Db          1 PGHGGIINTLQLYYCRVRGGRCAVLSCLPKEECIGKMSTRGRKCXRRKK 49
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Search completed: October 31, 2003, 14:05:03
Job time : 29 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 31, 2003, 13:59:27 ; Search time 40 Seconds
(without alignments)
161.083 Million cell updates/sec

Title: US-09-872-852-2
Perfect score: 367
Sequence: 1 MRIHYLLFALLFLFLVPVPG.....KEEQIGKCSTRGRKCCRRKK 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	113	30.8	64	2	A56128	lingual antimicrob
2	111	30.2	64	2	A47438	airway epithelial
3	108	29.4	65	2	C35947	crotamine 3 precur
4	108	29.4	65	2	A35947	crotamine 1 precur
5	103	28.1	65	2	JC5324	myotoxin a precurs
6	89	24.3	42	2	F45495	beta-defensin-6 -
7	83.5	22.8	64	2	B35947	crotamine 2 precur
8	75	20.4	38	2	B47753	beta-defensin-11 -
9	71	19.3	42	2	C45495	beta-defensin-3 -
10	69.5	18.9	45	2	A37909	myotoxin - eastern
11	69.5	18.9	95	1	WTRBM1	macrophage antibio
12	69	18.8	40	2	G45495	beta-defensin-7 -
13	69	18.8	40	2	I45495	beta-defensin-9 -
14	68	18.5	42	2	D47753	beta-defensin-13 -
15	66.5	18.1	43	1	CXRSCH	toxic peptide C -
16	65.5	17.8	42	1	CXRSMT	crotamine - tropic
17	65.5	17.8	51	2	D35947	crotamine 4 precur
18	65.5	17.8	95	1	WTRBM2	defensin CS-4 prec
19	62.5	17.0	42	1	MXRSMV	myotoxin a 6 - pra
20	61	16.6	122	2	JC6548	high sulfur protei
21	61	16.6	218	2	T22261	hypothetical prote
22	61	16.6	524	2	S38539	disintegrin-like m
23	61	16.6	670	2	I65967	disintegrin-like m
24	60.5	16.5	40	2	C39560	myotoxin a 5 - pra
25	60	16.3	32	2	E59076	defensin alpha-5 -
26	60	16.3	32	2	G59076	defensin alpha-7 -
27	60	16.3	33	2	D59076	defensin alpha-4 -
28	60	16.3	33	2	F59076	defensin alpha-6 -
29	60	16.3	855	2	T05981	hypothetical prote
30	59.5	16.2	260	2	AD2461	hypothetical prote
31	59.5	16.2	454	2	B82412	probable magnesium
32	59.5	16.2	1184	2	T09484	cartilage intermed
33	59	16.1	40	2	E45495	beta-defensin-5 -
34	59	16.1	177	2	S37650	high-sulfur kerati
35	59	16.1	263	2	S57346	interleukin 15 rec
36	58.5	15.9	43	2	A29089	myotoxin I - midge
37	58.5	15.9	45	2	S12909	myotoxin - western
38	58.5	15.9	88	2	H69475	hypothetical prote
39	58.5	15.9	112	2	A46717	colipase precursor
40	58.5	15.9	359	2	A96816	F9K20.25 [imported
41	58.5	15.9	705	2	S38066	probable finger pr
42	58	15.8	34	2	C49195	corticostatic pept
43	58	15.8	51	1	HSMSS1	protamine - mouse
44	58	15.8	51	2	S03997	protamine 1 - rat
45	58	15.8	152	2	I47109	high-sulfur wool m

ALIGNMENTS

RESULT 1
A56128
lingual antimicrobial peptide precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Nov-1999
C;Accession: A56128; B56128
R;Schonwetter, B.S.; Stolzenberg, E.D.; Zasloff, M.A.
Science 267, 1645-1648, 1995
A;Title: Epithelial antibiotics induced at sites of inflammation.
A;Reference number: A56128; MUID:95192714; PMID:7886453
A;Accession: A56128
A;Molecule type: mRNA
A;Residues: 1-64 <SCH>
A;Cross-references: GB:S76279; NID:g894208; PIDN:AAB33727.1; PID:g894209
A;Accession: B56128
A;Molecule type: protein
A;Residues: 23-64 <SC2>
C;Keywords: antibacterial; antifungal
F;1-20/Domain: signal sequence #status predicted <SIG>
F;23-64/Product: lingual antimicrobial peptide #status experimental <MAT>

Query Match 30.8%; Score 113; DB 2; Length 64;
Best Local Similarity 42.4%; Pred. No. 5e-06;
Matches 28; Conservative 3; Mismatches 33; Indels 2; Gaps 1;

```
Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||:|:|| ||||| |    | ||          ||   | |  : |     ||| |
Db          1 MRLHHLLLLALLFLVL--SAGSGFTQGVRNSQSCRRNKGICVPIRCPGSMRQIGTCLGAQV 58

Qy         61 KCCRRK 66
              ||||||
Db         59 KCCRRK 64
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RESULT 2
A47438
airway epithelial antimicrobial peptide TAP precursor - bovine
N;Alternate names: antimicrobial peptide, tracheal
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: A47438; A39397
R;Diamond, G.; Jones, D.E.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 4596-4600, 1993
A;Title: Airway epithelial cells are the site of expression of a mammalian antimicrobial
A;Reference number: A47438; MUID:93281626; PMID:8506305
A;Accession: A47438
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-64 <DIA>
A;Cross-references: GB:L13373; NID:g289395; PIDN:AAA72363.1; PID:g289396
R;Diamond, G.; Zasloff, M.; Eck, H.; Brasseur, M.; Maloy, W.L.; Bevins, C.L.
Proc. Natl. Acad. Sci. U.S.A. 88, 3952-3956, 1991

```
A;Title: Tracheal antimicrobial peptide, a cysteine-rich peptide from mammalian tracheal
A;Reference number: A39397; MUID:91219490; PMID:2023943
A;Accession: A39397
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-64 <DI2>
A;Cross-references: GB:M63023; NID:g2226433; PIDN:AAB61757.1; PID:g163740
C;Genetics:
A;Introns: 19/2
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-64/Product: airway epithelial antimicrobial peptide TAP #status predicted <MAT>

  Query Match             30.2%;  Score 111;  DB 2;  Length 64;
  Best Local Similarity   41.8%;  Pred. No. 8.4e-06;
  Matches   28;  Conservative    7;  Mismatches   28;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGH-GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||:|:|| ||||| |     |   |: | :    |  | | : |    :||| |  |
Db          1 MRLHHLLLALLFLVLSAWSGFTQGVGNPVS---CVRNKGICVPIRCPGSMKQIGTCVGRA 57

Qy         60 RKCCRRK 66
                ||||:|
Db         58 VKCCRKK 64


RESULT 3
C35947
crotamine 3 precursor - tropical rattlesnake
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1993
C;Accession: C35947
R;Smith, L.A.; Schmidt, J.J.
Toxicon 28, 575-585, 1990
A;Title: Cloning and nucleotide sequences of crotamine genes.
A;Reference number: A35947; MUID:90357261; PMID:2389256
A;Accession: C35947
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-65 <SMI>
C;Superfamily: crotamine

  Query Match             29.4%;  Score 108;  DB 2;  Length 65;
  Best Local Similarity   39.1%;  Pred. No. 1.9e-05;
  Matches   27;  Conservative    9;  Mismatches   21;  Indels   12;  Gaps    5;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGK--CS 56
              |:| ||||| |||  :  ||     |  ::  | ::|| |      |:|     ||  |
Db          1 MKILYLLFAFLFLAFLSEPG-----NAYKR--CHIKGGHCFPKGKICIPPSSDFGKMDCP 53

Qy         57 TRGRKCCRR 65
                | ||||::
Db         54 WR-RKCCKK 61


RESULT 4
A35947
crotamine 1 precursor - tropical rattlesnake
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1993
C;Accession: A35947
R;Smith, L.A.; Schmidt, J.J.
Toxicon 28, 575-585, 1990
A;Title: Cloning and nucleotide sequences of crotamine genes.
A;Reference number: A35947; MUID:90357261; PMID:2389256
A;Accession: A35947
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-65 <SMI>
C;Superfamily: crotamine

  Query Match             29.4%;  Score 108;  DB 2;  Length 65;
  Best Local Similarity   39.1%;  Pred. No. 1.9e-05;
  Matches   27;  Conservative    9;  Mismatches   21;  Indels   12;  Gaps    5;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGK--CS 56
              |:| ||||| |||  :  ||     |  ::  | ::|| |      |:|     ||  |
Db          1 MKILYLLFAFLFLAFLSEPG-----NAYKR--CHIKGGHCFPKEKICIPPSSDFGKMDCP 53

Qy         57 TRGRKCCRR 65
                | ||||::
Db         54 WR-RKCCKK 61


RESULT 5
JC5324
myotoxin a precursor - prairie rattlesnake
C;Species: Crotalus viridis viridis (prairie rattlesnake)
C;Date: 15-May-1997 #sequence_revision 18-Jul-1997 #text_change 02-Jul-1998
C;Accession: JC5324
R;Norris, J.W.; Fry, R.M.; Tu, A.T.
Biochem. Biophys. Res. Commun. 230, 607-610, 1997
A;Title: The nucleotide sequence of the translated and untranslated regions of a cDNA fc
A;Reference number: JC5324; MUID:97167753; PMID:9015371
A;Accession: JC5324
A;Molecule type: mRNA
A;Residues: 1-65 <NOR>
A;Experimental source: venom
A;Note: the authors translated the codon CAG for residue 27 as His and CTT for residue 4
C;Comment: This protein inhibits Ca2+ uptake into the sarcoplasmic reticulum by binding
C;Superfamily: crotamine
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-64/Product: myotoxin a #status predicted <MAT>

  Query Match             28.1%;  Score 103;  DB 2;  Length 65;
  Best Local Similarity   36.8%;  Pred. No. 7.1e-05;
  Matches   25;  Conservative   11;  Mismatches   22;  Indels   10;  Gaps    4;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGKCSTR 58
              |:| ||||| |||  :  ||     |  ::  |: :|| |      |:|    :||   |
Db          1 MKILYLLFAFLFLAFLSEPG-----NAYKQ--CQKKGGHCFPKEKICIPPSSDLGKMDCR 53

Qy         59 GR-KCCRR 65
                : |||::
Db         54 WKWKCCKK 61


RESULT 6
F45495
beta-defensin-6 - bovine
N;Alternate names: peptide BNBD-6
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C;Accession: F45495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: F45495
A;Molecule type: protein
A;Residues: 1-42 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
C;Keywords: antibacterial; disulfide bond; pyroglutamic acid
F;1-42/Product: beta-defensin-6 #status experimental <MA1>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

  Query Match             24.3%;  Score 89;  DB 2;  Length 42;
  Best Local Similarity   48.5%;  Pred. No. 0.002;
  Matches   16;  Conservative    3;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRR 65
              ||: || |  : |  :  ||| |  |  |||||
Db          9 CRIYGGFCVPIRCPGRTRQIGTCFGRPVKCCRR 41


RESULT 7
```

B35947
crotamine 2 precursor - tropical rattlesnake (fragment)
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1993
C;Accession: B35947
R;Smith, L.A.; Schmidt, J.J.
Toxicon 28, 575-585, 1990
A;Title: Cloning and nucleotide sequences of crotamine genes.
A;Reference number: A35947; MUID:90357261; PMID:2389256
A;Accession: B35947
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-64 <SMI>
C;Superfamily: crotamine

Query Match 22.8%; Score 83.5; DB 2; Length 64;
Best Local Similarity 32.8%; Pred. No. 0.012;
Matches 22; Conservative 9; Mismatches 27; Indels 9; Gaps 3;

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Qy          2 RIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGKCSTRG 59
              :| ||||| |||  :  ||     |  ::  | ::|| |      |:|     ||
Db          1 KILYLLFAFLFLAFLSEPG-----NAYKR--CHIKGGHCFPKEKICIPPSSDFGKMDCPW 53

Qy         60 RKCCRRK 66
              |:  :|
Db         54 RRKSLKK 60
```

RESULT 8
B47753
beta-defensin-11 - bovine
N;Alternate names: peptide BNBD-11
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Dec-1998
C;Accession: B47753
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: B47753
A;Molecule type: protein
A;Residues: 1-38 <SEL>
A;Note: sequence extracted from NCBI backbone (NCBIP:127961)
C;Keywords: antibacterial; disulfide bond
F;1-38/Product: beta-defensin-11 #status experimental <MA1>
F;5-34,12-27,17-35/Disulfide bonds: #status predicted

Query Match 20.4%; Score 75; DB 2; Length 38;
Best Local Similarity 46.9%; Pred. No. 0.074;
Matches 15; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

```
Qy         33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCR 64
              ||  || |  : |     ||| |  |  ||||
Db          5 CRRNGGVCIPIRCPGPMRQIGTCFGRPVKCCR 36
```

RESULT 9
C45495
beta-defensin-3 - bovine
N;Alternate names: peptide BNBD-3
N;Contains: beta-defensin-2
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C;Accession: C45495; B45495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: C45495
A;Molecule type: protein
A;Residues: 1-42 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
A;Accession: B45495
A;Molecule type: protein
A;Residues: 3-42 <SE2>
A;Note: sequence extracted from NCBI backbone (NCBIP:127952)
C;Keywords: antibacterial; disulfide bond; pyroglutamic acid
F;1-42/Product: beta-defensin-3 #status experimental <MA1>
F;3-42/Product: beta-defensin-2 #status experimental <MA2>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 19.3%; Score 71; DB 2; Length 42;
Best Local Similarity 40.6%; Pred. No. 0.23;
Matches 13; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

```
Qy         33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCR 64
              ||:  | |  : |  :  ||| |     ||||
Db          9 CRINRGFCVPIRCPGRTRQIGTCFGPRIKCCR 40
```

RESULT 10
A37909
myotoxin - eastern diamondback rattlesnake
C;Species: Crotalus adamanteus (eastern diamondback rattlesnake)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 11-Nov-1994
C;Accession: A37909
R;Samejima, Y.; Aoki, Y.; Mebs, D.
Toxicon 29, 461-468, 1991
A;Title: Amino acid sequence of a myotoxin from venom of the eastern diamondback rattlesr
A;Reference number: A37909; MUID:91320359; PMID:1862521
A;Accession: A37909
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-45 <SAM>
C;Superfamily: crotamine
C;Keywords: myotoxin

Query Match 18.9%; Score 69.5; DB 2; Length 45;
Best Local Similarity 38.9%; Pred. No. 0.37;
Matches 14; Conservative 4; Mismatches 15; Indels 3; Gaps 2;

```
Qy         33 CRVRGGRC--AVLSCLPKEEQIGKCSTRGR-KCCRR 65
              |  :|| |    : |||     ||   | | |||::
Db          4 CHKKGGHCFPKTVICLPPSSDFGKMDCRWRWKCCKK 39
```

RESULT 11
WTRBM1
macrophage antibiotic peptide MCP-1 - rabbit
N;Alternate names: antiadrenocorticotropin, corticostatic peptide CS-3; defensin
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1985 #sequence_revision 23-Feb-1996 #text_change 18-Jun-1999
C;Accession: A45811; A01647; A22569; B49195
R;Ganz, T.; Rayner, J.R.; Valore, E.V.; Tumolo, A.; Talmadge, K.; Fuller, F.
J. Immunol. 143, 1358-1365, 1989
A;Title: The structure of the rabbit macrophage defensin genes and their organ-specific e
A;Reference number: A45811; MUID:89309825; PMID:2745983
A;Accession: A45811
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <GAN>
A;Cross-references: GB:M28072; NID:g165473; PIDN:AAA31388.1; PID:g165474
R;Selsted, M.E.; Brown, D.M.; DeLange, R.J.; Lehrer, R.I.
J. Biol. Chem. 258, 14485-14489, 1983
A;Title: Primary structures of MCP-1 and MCP-2, natural peptide antibiotics of rabbit lur
A;Reference number: A01647; MUID:84061901; PMID:6643497
A;Accession: A01647
A;Molecule type: protein
A;Residues: 63-95 <SE1>
R;Selsted, M.E.; Brown, D.M.; DeLange, R.J.; Harwig, S.S.L.; Lehrer, R.I.
J. Biol. Chem. 260, 4579-4584, 1985
A;Title: Primary structures of six antimicrobial peptides of rabbit peritoneal neutrophil
A;Reference number: A22569; MUID:85182561; PMID:3988726
A;Accession: A22569
A;Molecule type: protein

A;Residues: 63-95 <SB2>
A;Experimental source: peritoneal neutrophils
R;Zhu, Q.; Solomon, S.
Endocrinology 130, 1413-1423, 1992
A;Title: Isolation and mode of action of rabbit corticostatic (antiadrenocorticotropin)
A;Reference number: A49195; MUID:92164536; PMID:1311240
A;Accession: B49195
A;Status: preliminary
A;Molecule type: protein
A;Residues: 63-95 <ZHU>
A;Note: sequence extracted from NCBI backbone (NCBIP:85970)
C;Comment: This peptide is active against some fungi and gram-positive bacteria in vitro
C;Superfamily: mammalian defensin
C;Keywords: antibacterial
F;65-93,67-82,72-92/Disulfide bonds: #status predicted

Query Match 18.9%; Score 69.5; DB 1; Length 95;
Best Local Similarity 48.3%; Pred. No. 0.68;
Matches 14; Conservative 2; Mismatches 10; Indels 3; Gaps 1;

```
Qy         40 CAVLSCLPKEEQIGKCSTRGR---KCCRR 65
              |    |||:| : | |  |||    ||||
Db         67 CRRALCLPRERRAGFCRIRGRIHPLCCRR 95
```

RESULT 12
G45495
beta-defensin-7 - bovine
N;Alternate names: peptide BNBD-7
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C;Accession: G45495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: G45495
A;Molecule type: protein
A;Residues: 1-40 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
C;Keywords: antibacterial; disulfide bond; pyroglutamic acid
F;1-40/Product: beta-defensin-7 #status experimental <MA1>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 18.8%; Score 69; DB 2; Length 40;
Best Local Similarity 40.6%; Pred. No. 0.38;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

```
Qy         33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCR 64
              ||:  | |  : |     ||| |     ||||
Db          9 CRINRGFCVPIRCPGHRRQIGTCLGPRIKCCR 40
```

RESULT 13
I45495
beta-defensin-9 - bovine
N;Alternate names: peptide BNBD-9
N;Contains: beta-defensin-8
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 22-Apr-1995
C;Accession: I45495; H45495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: I45495
A;Molecule type: protein
A;Residues: 1-40 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
A;Accession: H45495
A;Molecule type: protein
A;Residues: 3-40 <SE2>
A;Note: sequence extracted from NCBI backbone (NCBIP:127958)
C;Keywords: pyroglutamic acid
F;1-40/Product: beta-defensin-9 #status experimental <MA1>
F;3-40/Product: beta-defensin-8 #status experimental <MA2>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

Query Match 18.8%; Score 69; DB 2; Length 40;
Best Local Similarity 40.6%; Pred. No. 0.38;
Matches 13; Conservative 2; Mismatches 17; Indels 0; Gaps 0;

```
Qy         33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCR 64
              ||:  | |  : |     ||| |     ||||
Db          9 CRINRGFCVPIRCPGHRRQIGTCLGPQIKCCR 40
```

RESULT 14
D47753
beta-defensin-13 - bovine
N;Alternate names: peptide BNBD-13
N;Contains: beta-defensin-12
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 22-Apr-1995
C;Accession: D47753; C47753
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: D47753
A;Molecule type: protein
A;Residues: 1-42 <SEL>
A;Note: sequence extracted from NCBI backbone (NCBIP:127963)
A;Accession: C47753
A;Molecule type: protein
A;Residues: 5-42 <SE2>
A;Note: sequence extracted from NCBI backbone (NCBIP:127962)
C;Keywords: disulfide bond
F;1-42/Product: beta-defensin-13 #status experimental <MA1>
F;5-42/Product: beta-defensin-12 #status experimental <MA2>
F;9-38,16-31,21-39/Disulfide bonds: #status experimental

Query Match 18.5%; Score 68; DB 2; Length 42;
Best Local Similarity 43.8%; Pred. No. 0.51;
Matches 14; Conservative 1; Mismatches 17; Indels 0; Gaps 0;

```
Qy         33 CRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCR 64
              |   || |  : |     ||| |  |  ||||
Db          9 CGRNGGVCIPIRCPVPMRQIGTCFGRPVKCCR 40
```

RESULT 15
CXRSCH
toxic peptide C - southern Pacific rattlesnake
C;Species: Crotalus viridis helleri (southern Pacific rattlesnake)
C;Date: 31-May-1979 #sequence_revision 08-Oct-1981 #text_change 23-Aug-1996
C;Accession: A01737
R;Maeda, N.; Tamiya, N.; Pattabhiraman, T.R.; Russell, F.E.
Toxicon 16, 431-441, 1978
A;Title: Some chemical properties of the venom of the rattlesnake, Crotalus viridis hell
A;Reference number: A01737; MUID:79015339; PMID:694946
A;Accession: A01737
A;Molecule type: protein
A;Residues: 1-43 <MAE>
C;Superfamily: crotamine
C;Keywords: myotoxin; venom
F;4-36,11-30,18-37/Disulfide bonds: #status predicted

Query Match 18.1%; Score 66.5; DB 1; Length 43;
Best Local Similarity 36.1%; Pred. No. 0.78;
Matches 13; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

```
Qy         33 CRVRGGRC--AVLSCLPKEEQIGKCSTRGR-KCCRR 65
              |  :|| |    : |||     ||   | : |||::
```

Db 4 CHKKGGHCFPKTVICLPPSSDFGKMDCRWKWKCCKK 39

Search completed: October 31, 2003, 14:04:29
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 31, 2003, 13:55:57 ; Search time 23 Seconds
(without alignments)
136.991 Million cell updates/sec

Title: US-09-872-852-2
Perfect score: 367
Sequence: 1 MRIHYLLFALLFLFLVPVPG.....KEEQIGKCSTRGRKCCRRKK 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	367	100.0	67	1	D103_HUMAN	P81534 homo sapien
2	133	36.2	64	1	BD02_HUMAN	O15263 homo sapien
3	121.5	33.1	63	1	BD03_MOUSE	Q9wtl0 mus musculu
4	119	32.4	64	1	BD01_PIG	O62697 sus scrofa
5	116	31.6	64	1	EAP_BOVIN	O02775 bos taurus
6	113	30.8	64	1	LAP_BOVIN	Q28880 bos taurus
7	111	30.2	64	1	TAP_BOVIN	P25068 bos taurus
8	108	29.4	65	1	MYX1_CRODU	P24331 crotalus du
9	108	29.4	65	1	MYX3_CRODU	P24333 crotalus du
10	106	28.9	64	1	BD05_BOVIN	P46163 bos taurus
11	100.5	27.4	63	1	BD02_RAT	O88514 rattus norv
12	100	27.2	64	1	BD01_CAPHI	O97946 capra hircu
13	98	26.7	64	1	BD02_SHEEP	O19039 ovis aries
14	94	25.6	53	1	BDC7_BOVIN	O18815 bos taurus
15	93	25.3	64	1	BD01_SHEEP	O19038 ovis aries
16	92	25.1	63	1	BD04_BOVIN	P46162 bos taurus
17	90.5	24.7	63	1	BD04_MOUSE	P82019 mus musculu
18	89	24.3	42	1	BD06_BOVIN	P46164 bos taurus
19	89	24.3	69	1	BD01_RAT	O89117 rattus norv
20	85	23.2	69	1	BD01_MOUSE	P56386 mus musculu
21	84	22.9	55	1	BD09_BOVIN	P46167 bos taurus
22	84	22.9	57	1	BD03_BOVIN	P46161 bos taurus
23	83.5	22.8	64	1	MYX2_CRODU	P24332 crotalus du
24	82.5	22.5	64	1	GLL3_CHICK	P46158 gallus gall
25	78.5	21.4	65	1	AMP1_MELGA	P80391 meleagris g
26	75	20.4	38	1	BD11_BOVIN	P46169 bos taurus
27	74	20.2	68	1	BD01_HUMAN	Q09753 homo sapien
28	73.5	20.0	64	1	AMP2_MELGA	P80392 meleagris g
29	73.5	20.0	65	1	GLL1_CHICK	P46156 gallus gall
30	73.5	20.0	71	1	BD02_MOUSE	P82020 mus musculu
31	71	19.3	40	1	BD02_BOVIN	P46160 bos taurus
32	69.5	18.9	45	1	MYX_CROAD	P24330 crotalus ad
33	69.5	18.9	95	1	DEF3_RABIT	P01376 oryctolagus
34	69	18.8	38	1	BD08_BOVIN	P46166 bos taurus
35	69	18.8	40	1	BD07_BOVIN	P46165 bos taurus
36	68	18.5	38	1	BD12_BOVIN	P46170 bos taurus
37	68	18.5	42	1	BD13_BOVIN	P46171 bos taurus
38	66.5	18.1	43	1	MYXC_CROVH	P01477 crotalus vi
39	66.5	18.1	65	1	D106_HUMAN	Q8n104 homo sapien
40	66.5	18.1	73	1	D108_HUMAN	Q8net1 homo sapien
41	65.5	17.8	42	1	MYXC_CRODU	P01475 crotalus du
42	65.5	17.8	51	1	MYX4_CRODU	P24334 crotalus du
43	65.5	17.8	95	1	DEF4_RABIT	P01377 oryctolagus
44	65	17.7	68	1	BD01_MACMU	O18794 macaca mula
45	64	17.4	116	1	MCS_HUMAN	P49901 homo sapien

ALIGNMENTS

RESULT 1
D103_HUMAN
ID D103_HUMAN STANDARD; PRT; 67 AA.
AC P81534; Q9NPF6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Beta-defensin 3 precursor (BD-3) (hBD-3) (Beta-defensin 103) (Defensin
DE like protein).
GN DEFB103 OR DEFB3 OR BD3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY,
RP INDUCTION, AND MASS SPECTROMETRY.
RC TISSUE=Keratinocytes, Lung epithelial cells, and Tracheal epithelium;
RX MEDLINE=21101950; PubMed=11085990;
RA Harder J., Bartels J., Christophers E., Schroeder J.-M.;
RT "Isolation and characterization of human deta-defensin-3, a novel
RT human inducible peptide antibiotic.";
RL J. Biol. Chem. 276:5707-5713(2001).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=21558153; PubMed=11702237;
RA Garcia J.-R., Jaumann F., Schulz S., Krause A., Rodriguez-Jimenez J.,
RA Forssmann U., Adermann K., Kluver E., Vogelmeier C., Becker D.,
RA Hedrich R., Forssmann W.-G., Bals R.;
RT "Identification of a novel, multifunctional beta-defensin (human
RT beta-defensin 3) with specific antimicrobial activity. Its
RT interaction with plasma membranes of Xenopus oocytes and the
RT induction of macrophage chemoattraction.";
RL Cell Tissue Res. 306:257-264(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125233; PubMed=11223260;
RA Jia H.P., Schutte B.C., Schudy A., Linzmeier R., Guthmiller J.M.,
RA Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz T.,
RA McCray P.B. Jr.;
RT "Discovery of new human defensins using a genomics-based approach.";
RL Gene 263:211-218(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Imai Y.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S.,
RA Jaspers S., Whitmore T., Fox B., Gosink J., Rixon M., Gao Z.,
RA Haldeman B., O'Hara P.;
RT "EST and genomic database mining yield novel human and mouse
RT beta-defensins.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: EXHIBITS ANTIMICROBIAL ACTIVITY AGAINST GRAM-POSITIVE
CC BACTERIA S.AUREUS AND S.PYOGENES, GRAM-NEGATIVE BACTERIA

```
CC       P.AERUGINOSA AND E.COLI AND THE YEAST C.ALBICANS. KILLS
CC       MULTIRESISTANT S.AUREUS AND VANCOMYCIN-RESISTENT E.FAECIUM. NO
CC       SIGNIFICANT HEMOLYTIC ACTIVITY WAS OBSERVED.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SKIN AND TONSILS, AND TO A
CC       LESSER EXTENT IN TRACHEA, UTERUS, KIDNEY, THYMUS, ADENOID, PHARYNX
CC       AND TONGUE. LOW EXPRESSION IN SALIVARY GLAND, BONE MARROW, COLON,
CC       STOMACH, POLYP AND LARYNX. NO EXPRESSION IN SMALL INTESTINE.
CC   -!- INDUCTION: BY INFECTION OF BACTERIA AND BY INTERFERON GAMMA.
CC   -!- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ237673; CAC03097.1; -.
DR   EMBL; AF295370; AAG02237.1; -.
DR   EMBL; AF217245; AAF73853.1; -.
DR   EMBL; AB037972; BAB40572.1; -.
DR   EMBL; AF301470; AAG22030.1; -.
DR   PDB; 1KJ6; 20-MAR-02.
DR   Genew; HGNC:15967; DEFB103.
DR   MIM; 606611; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0008224; F:Gram-positive antibacterial peptide activity; TAS.
DR   GO; GO:0006965; P:anti-Gram-positive bacterial polypeptide in. . .; TAS.
DR   InterPro; IPR001855; Defensin_beta.
DR   Pfam; PF00711; Defensin_beta; 1.
KW   Antibiotic; Signal; 3D-structure.
FT   SIGNAL       1     22
FT   CHAIN       23     67       BETA-DEFENSIN 3.
FT   DISULFID    33     62       BY SIMILARITY.
FT   DISULFID    40     55       BY SIMILARITY.
FT   DISULFID    45     63       BY SIMILARITY.
SQ   SEQUENCE   67 AA;  7697 MW;  54266DE1C90D4B65 CRC64;

  Query Match           100.0%;  Score 367;  DB 1;  Length 67;
  Best Local Similarity 100.0%;  Pred. No. 1.9e-35;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67


RESULT 2
BD02_HUMAN
ID   BD02_HUMAN     STANDARD;      PRT;    64 AA.
AC   O15263;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Beta-defensin 2 precursor (hBD-2) (Skin-antimicrobial peptide 1)
DE   (SAP1).
GN   DEFB4 OR DEFB2 OR DEFB102.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=97345625; PubMed=9202117;
RA   Harder J., Bartels J.H., Christophers E., Schroeder J.-M.;
RT   "A peptide antibiotic from human skin.";
RL   Nature 387:861-861(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=99051334; PubMed=9831658;
RA   Liu L., Wang L., Jia H.P., Zhao C., Heng H.H.Q., Schutte B.C.,
RA   McCray P.B. Jr., Ganz T.;
RT   "Structure and mapping of the human beta-defensin HBD-2 gene and its
RT   expression at sites of inflammation.";
RL   Gene 222:237-244(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20072673; PubMed=10603376;
RA   Diamond G., Kaiser V., Rhodes J., Russell J.P., Bevins C.L.;
RT   "Transcriptional regulation of beta-defensin gene expression in
RT   tracheal epithelial cells.";
RL   Infect. Immun. 68:113-119(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Harder J., Schroeder J.M.;
RT   "Transcriptional regulation of the human beta-defensin-2 (hBD-2).";
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SYNTHESIS OF 24-64.
RX   MEDLINE=22007551; PubMed=12010514;
RA   Kluever E., Schulz A., Forssmann W.-G., Adermann K.;
RT   "Chemical synthesis of beta-defensins and LEAP-1/hepcidin.";
RL   J. Pept. Res. 59:241-248(2002).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
RX   MEDLINE=20490730; PubMed=10906336;
RA   Hoover D.M., Rajashankar K.R., Blumenthal R., Puri A., Oppenheim J.J.,
RA   Chertov O., Lubkowski J.;
RT   "The structure of human beta-defensin-2 shows evidence of higher
RT   order oligomerization.";
RL   J. Biol. Chem. 275:32911-32918(2000).
RN   [7]
RP   STRUCTURE BY NMR OF 28-64.
RX   MEDLINE=21571984; PubMed=11714914;
RA   Bauer F., Schweimer K., Kluver E., Conejo-Garcia J.R.,
RA   Forssmann W.-G., Rosch P., Adermann K., Sticht H.;
RT   "Structure determination of human and murine beta-defensins reveals
RT   structural conservation in the absence of significant sequence
RT   similarity.";
RL   Protein Sci. 10:2470-2479(2001).
CC   -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE SKIN AND RESPIRATORY TRACT.
CC   -!- INDUCTION: By inflammation.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z71389; CAA95992.1; -.
DR   EMBL; AF040153; AAC33549.1; -.
DR   EMBL; AF071216; AAC69554.1; -.
DR   EMBL; AJ000152; CAB65126.1; -.
DR   PDB; 1FD3; 01-NOV-00.
DR   PDB; 1FD4; 01-NOV-00.
DR   PDB; 1E4Q; 26-NOV-01.
DR   PDB; 1FQQ; 31-DEC-02.
DR   Genew; HGNC:2767; DEFB4.
DR   MIM; 602215; -.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
```

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DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0009613; P:response to pest/pathogen/parasite; TAS.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal; 3D-structure.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24     64       BETA-DEFENSIN 2.
FT   DISULFID     31     60
FT   DISULFID     38     53
FT   DISULFID     43     61
FT   STRAND       26     26
FT   HELIX        28     33
FT   TURN         34     35
FT   STRAND       37     39
FT   TURN         45     46
FT   STRAND       48     52
FT   TURN         56     57
FT   STRAND       59     62
SQ   SEQUENCE   64 AA;  7038 MW;  05D6454CE7ACD10E CRC64;

  Query Match             36.2%;  Score 133;  DB 1;  Length 64;
  Best Local Similarity   42.4%;  Pred. No. 1.1e-08;
  Matches   28;  Conservative   12;  Mismatches   22;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPG-HGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||: ||||: ||:||:|:||  ||| : :    |   |  |  : |  : :||| |   |
Db          1 MRVLYLLFSFLFIFLMPLPGVFGGIGDPVT---CLKSGAICHPVFCPRRYKQIGTCGLPG 57

Qy         60 RKCCRR 65
                |||::
Db         58 TKCCKK 63


RESULT 3
BD03_MOUSE
ID   BD03_MOUSE     STANDARD;      PRT;    63 AA.
AC   Q9WTL0;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Beta-defensin 3 precursor (BD-3) (mBD-3).
GN   DEFB3 OR BD3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, INDUCTION, AND TISSUE SPECIFICITY.
RC   STRAIN=C57BL/6; TISSUE=Lung;
RX   MEDLINE=99307216; PubMed=10377137;
RA   Bals R., Wang X., Meegalla R.L., Wattler S., Weiner D.J., Nehls M.C.,
RA   Wilson J.M.;
RT   "Mouse beta-defensin 3 is an inducible antimicrobial peptide expressed
RT   in the epithelia of multiple organs.";
RL   Infect. Immun. 67:3542-3547(1999).
RN   [2]
RP   TISSUE SPECIFICITY.
RC   STRAIN=C57BL/6, 129/SvJ, and FVB; TISSUE=Lung;
RX   MEDLINE=20517883; PubMed=10922379;
RA   Jia H.P., Wowk S.A., Schutte B.C., Lee S.K., Vivado A., Tack B.F.,
RA   Bevins C.L., McCray P.B. Jr.;
RT   "A novel murine beta-defensin expressed in tongue, esophagus, and
RT   trachea.";
RL   J. Biol. Chem. 275:33314-33320(2000).
CC   -!- FUNCTION: ANTIMICROBIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIA
CC       E.COLI AND P.AERUGINOSA.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SALIVARY GLANDS,
CC       EPIDIDYMIS, OVARY AND PANCREAS AND TO A LESSER EXTENT IN LUNG,
CC       LIVER AND BRAIN. LOW OR NO EXPRESSION IN SKELETAL MUSCLE AND
CC       TONGUE.
CC   -!- INDUCTION: By bacterial infection.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF093245; AAD29573.1; -.
DR   EMBL; AF092929; AAD29572.1; -.
DR   HSSP; P46170; 1BNB.
DR   MGD; MGI:1351612; Defb3.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Cleavage on pair of basic residues; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   PROPEP       21     22       POTENTIAL.
FT   CHAIN        23     63       BETA-DEFENSIN 3.
FT   DISULFID     31     59       BY SIMILARITY.
FT   DISULFID     38     52       BY SIMILARITY.
FT   DISULFID     42     60       BY SIMILARITY.
SQ   SEQUENCE   63 AA;  7126 MW;  9D59BC8AD16EA330 CRC64;

  Query Match             33.1%;  Score 121.5;  DB 1;  Length 63;
  Best Local Similarity   43.9%;  Pred. No. 2.2e-07;
  Matches   29;  Conservative    4;  Mismatches   30;  Indels    3;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              |||||||||| | : | |        ||       |  :||||    |:    ||| |
Db          1 MRIHYLLFAFLLVLLSPPAAFSKKIN--NPVSCLRKGGRC-WNRCIGNTRQIGSCGVPFL 57

Qy         61 KCCRRK 66
                |||:||
Db         58 KCCKRK 63


RESULT 4
BD01_PIG
ID   BD01_PIG       STANDARD;      PRT;    64 AA.
AC   O62697;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Beta-defensin 1 precursor (BD-1) (Defensin, beta 1).
GN   DEFB1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98196859; PubMed=9537511;
RA   Zhang G., Wu H., Shi J., Ganz T., Ross C., Blecha F.;
RT   "Molecular cloning and tissue expression of porcine beta-defensin-1.";
RL   FEBS Lett. 424:37-40(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99377035; PubMed=10446172;
RA   Zhang G., Hiraiwa H., Yasue H., Wu H., Ross C.R., Troyer D.,
RA   Blecha F.;
RT   "Cloning and characterization of the gene for a new epithelial
RT   beta-defensin. Genomic structure, chromosomal localization, and
RT   evidence for its constitutive expression.";
RL   J. Biol. Chem. 274:24031-24037(1999).
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
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CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF031666; AAC39175.1; -.
DR   EMBL; AF132038; AAD51137.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   PROPEP       21     23       BY SIMILARITY.
FT   CHAIN        24     64       BETA-DEFENSIN 1.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7066 MW;  0A4B7494BA3E337A CRC64;

  Query Match             32.4%;  Score 119;  DB 1;  Length 64;
  Best Local Similarity   40.9%;  Pred. No. 4.3e-07;
  Matches   27;  Conservative    6;  Mismatches   31;  Indels    2;  Gaps    1;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||:| ||   | : |:||||   : |      |    | |    | || :||| |
Db          1 MRLHRLLLVFLLMVLLPVPGL--LKNIGNSVSCLRNKGVCMPGKCAPKMKQIGTCGMPQV 58

Qy         61 KCCRRK 66
              |||:||
Db         59 KCCKRK 64


RESULT 5
EAP_BOVIN
ID   EAP_BOVIN      STANDARD;      PRT;    64 AA.
AC   O02775;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Enteric beta-defensin precursor.
GN   EBD.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98147718; PubMed=9488394;
RA   Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA   Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA   Wines M., Hwang S., Bevins C.L.;
RT   "Enteric beta-defensin: molecular cloning and characterization of a
RT   gene with inducible intestinal epithelial cell expression associated
RT   with Cryptosporidium parvum infection.";
RL   Infect. Immun. 66:1045-1056(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96014297; PubMed=8589529;
RA   Gallagher D.S. Jr., Ryan A.M., Diamond G., Bevins C.L., Womack J.E.;
RT   "Somatic cell mapping of beta-defensin genes to cattle syntenic group
RT   U25 and fluorescence in situ localization to chromosome 27.";
RL   Mamm. Genome 6:554-556(1995).
CC   -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: INDUCIBLY EXPRESSED IN ENTERIC EPITHELIAL
CC       CELLS.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC       SUBFAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF000362; AAC48805.1; -.
DR   EMBL; AF016539; AAC48804.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27     64       ENTERIC BETA-DEFENSIN.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7126 MW;  7E8642AE6F7A6068 CRC64;

  Query Match             31.6%;  Score 116;  DB 1;  Length 64;
  Best Local Similarity   44.6%;  Pred. No. 9.4e-07;
  Matches   29;  Conservative    4;  Mismatches   28;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGH-GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||:|:||  |||| |    |  || | |    ||:  | |  : |     ||| | |
Db          1 MRLHHLLLLTLLFLVLSAGSGFTQGISNPLS---CRLNRGICVPIRCPGNLRQIGTCFTPS 57

Qy         60 RKCCR 64
              ||||
Db         58 VKCCR 62


RESULT 6
LAP_BOVIN
ID   LAP_BOVIN      STANDARD;      PRT;    64 AA.
AC   Q28880; Q28202;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Lingual antimicrobial peptide precursor.
GN   LAP.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Tongue epithelium;
RX   MEDLINE=95192714; PubMed=7886453;
RA   Schonwetter B.S., Stolzenberg E.D., Zasloff M.A.;
RT   "Epithelial antibiotics induced at sites of inflammation.";
RL   Science 267:1645-1648(1995).
RN   [2]
RP   SEQUENCE OF 3-64 FROM N.A.
RX   MEDLINE=96201562; PubMed=8613361;
RA   Russell J.P., Diamond G., Tarver A.P., Scanlin T.F., Bevins C.L.;
RT   "Coordinate induction of two antibiotic genes in tracheal epithelial
RT   cells exposed to the inflammatory mediators lipopolysaccharide and
RT   tumor necrosis factor alpha.";
RL   Infect. Immun. 64:1565-1568(1996).
CC   -!- FUNCTION: SHOWS A BROAD SPECTRUM OF ANTIBACTERIAL AND ANTIFUNGAL
CC       ACTIVITIES.
CC   -!- TISSUE SPECIFICITY: IN MANY OF THE EXPOSED EPITHELIAL SURFACES
CC       INCLUDING CONJUCTIVAE, BRONCHI, COLON, URINARY TRACT AND TRACHEA.
CC   -!- DEVELOPMENTAL STAGE: NOT FOUND IN FETUS.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
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CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S76279; AAB33727.1; -.
DR   EMBL; U48357; AAB05401.1; -.
DR   PIR; A56128; A56128.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal; Fungicide.
FT   SIGNAL        1     19       POTENTIAL.
FT   PEPTIDE      20     64       LINGUAL ANTIMICROBIAL PEPTIDE.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
FT   CONFLICT     20     20       G -> R (IN REF. 2).
SQ   SEQUENCE   64 AA;  7041 MW;  BD24CDA3B3912F8F CRC64;

  Query Match             30.8%;  Score 113;  DB 1;  Length 64;
  Best Local Similarity   42.4%;  Pred. No. 2.1e-06;
  Matches   28;  Conservative    3;  Mismatches   33;  Indels    2;  Gaps    1;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||:|:|| ||||| |    | |          ||   | |  : |     ||| |
Db          1 MRLHHLLLLALLFLVL--SAGSGFTQGVRNSQSCRRNKGICVPIRCPGSMRQIGTCLGAQV 58

Qy         61 KCCRRK 66
              ||||||
Db         59 KCCRRK 64


RESULT 7
TAP_BOVIN
ID   TAP_BOVIN      STANDARD;      PRT;    64 AA.
AC   P25068; O97532;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Tracheal antimicrobial peptide precursor (TAP).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-59.
RC   TISSUE=Tracheal epithelium;
RX   MEDLINE=91219490; PubMed=2023943;
RA   Diamond G., Zasloff M., Eck H., Brasseur M., Maloy W.L., Bevins C.L.;
RT   "Tracheal antimicrobial peptide, a cysteine-rich peptide from
RT   mammalian tracheal mucosa: peptide isolation and cloning of a cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:3952-3956(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RX   MEDLINE=93281626; PubMed=8506305;
RA   Diamond G., Jones D.E., Bevins C.L.;
RT   "Airway epithelial cells are the site of expression of a mammalian
RT   antimicrobial peptide gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:4596-4600(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ryan L.K., Rhodes J., Bhat M., Diamond G.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: HAS ANTIBACTERIAL ACTIVITY IN VITRO AGAINST ESCHERICHIA
CC       COLI, STAPHYLOCOCCUS AUREUS, KLEBSIELLA PNEUMONIA, AND PSEUDOMONAS
CC       AERUGINOSA. IN ADDITION, THE PEPTIDE IS ACTIVE AGAINST CANDIDA
CC       ALBICANS, INDICATING A BROAD SPECTRUM OF ACTIVITY.
CC   -!- TISSUE SPECIFICITY: TRACHEAL EPITHELIUM.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M63023; AAB61757.1; -.
DR   EMBL; L13373; AAA72363.1; -.
DR   EMBL; AF014106; AAD01521.1; -.
DR   PIR; A47438; A47438.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27     64       TRACHEAL ANTIMICROBIAL PEPTIDE.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
FT   CONFLICT     18     18       W -> S (IN REF. 3).
FT   CONFLICT     46     46       S -> N (IN REF. 3).
SQ   SEQUENCE   64 AA;  6953 MW;  68617B95E02918E6 CRC64;

  Query Match             30.2%;  Score 111;  DB 1;  Length 64;
  Best Local Similarity   41.8%;  Pred. No. 3.5e-06;
  Matches   28;  Conservative    7;  Mismatches   28;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGH-GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||:|:|| ||||| |    |   |: | :    |     | |  : |    :||| |  |
Db          1 MRLHHLLLLALLFLVLSAWSGFTQGVGNPVS---CVRNKGICVPIRCPGSMKQIGTCVGRA 57

Qy         60 RKCCRRK 66
                ||||:|
Db         58 VKCCRKK 64


RESULT 8
MYX1_CRODU
ID   MYX1_CRODU     STANDARD;      PRT;    65 AA.
AC   P24331;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Myotoxin 1 precursor (Crotamine 1).
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=90357261; PubMed=2389256;
RA   Smith L.A., Schmidt J.J.;
RT   "Cloning and nucleotide sequences of crotamine genes.";
RL   Toxicon 28:575-585(1990).
CC   -!- FUNCTION: Causes severe muscle necrosis by a non-enzymatic
CC       mechanism. Acts extremely rapidly and serves two primary
CC       functions: limit the flight of prey by causing instantaneous
CC       paralysis of the hind limbs and promote rapid death by paralysis
CC       of the diaphragm.
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CC   -!- SIMILARITY: BELONGS TO THE MYOTOXIN FAMILY OF SNAKE TOXINS.
DR   PIR; A35947; A35947.
DR   InterPro; IPR000881; Myotoxin.
DR   Pfam; PF00819; Myotoxins; 1.
DR   ProDom; PD005972; Myotoxin; 1.
DR   PROSITE; PS00459; MYOTOXINS; 1.
KW   Toxin; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23     64       MYOTOXIN 1.
FT   DISULFID     26     58       BY SIMILARITY.
FT   DISULFID     33     52       BY SIMILARITY.
FT   DISULFID     40     59       BY SIMILARITY.
SQ   SEQUENCE   65 AA;  7443 MW;  A1B75A6CC7359806 CRC64;

  Query Match             29.4%;  Score 108;  DB 1;  Length 65;
  Best Local Similarity   39.1%;  Pred. No. 7.9e-06;
  Matches   27;  Conservative    9;  Mismatches   21;  Indels   12;  Gaps    5;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGK--CS 56
              |:| ||||| |||  :  ||     |  ::  | ::|| |      |:|     ||  |
Db          1 MKILYLLFAFLFLAFLSEPG-----NAYKR--CHIKGGHCFPKEKICIPPSSDFGKMDCP 53

Qy         57 TRGRKCCRR 65
                | ||||::
Db         54 WR-RKCCKK 61


RESULT 9
MYX3_CRODU
ID   MYX3_CRODU     STANDARD;      PRT;    65 AA.
AC   P24333;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Myotoxin 3 precursor (Crotamine 3).
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=90357261; PubMed=2389256;
RA   Smith L.A., Schmidt J.J.;
RT   "Cloning and nucleotide sequences of crotamine genes.";
RL   Toxicon 28:575-585(1990).
CC   -!- FUNCTION: Causes severe muscle necrosis by a non-enzymatic
CC       mechanism. Acts extremely rapidly and serves two primary
CC       functions: limit the flight of prey by causing instantaneous
CC       paralysis of the hind limbs and promote rapid death by paralysis
CC       of the diaphragm.
CC   -!- SIMILARITY: BELONGS TO THE MYOTOXIN FAMILY OF SNAKE TOXINS.
DR   PIR; C35947; C35947.
DR   InterPro; IPR000881; Myotoxin.
DR   Pfam; PF00819; Myotoxins; 1.
DR   ProDom; PD005972; Myotoxin; 1.
DR   PROSITE; PS00459; MYOTOXINS; 1.
KW   Toxin; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23     64       MYOTOXIN 3.
FT   DISULFID     26     58       BY SIMILARITY.
FT   DISULFID     33     52       BY SIMILARITY.
FT   DISULFID     40     59       BY SIMILARITY.
SQ   SEQUENCE   65 AA;  7371 MW;  A1B75A6CC515BA06 CRC64;

  Query Match             29.4%;  Score 108;  DB 1;  Length 65;
  Best Local Similarity   39.1%;  Pred. No. 7.9e-06;
  Matches   27;  Conservative    9;  Mismatches   21;  Indels   12;  Gaps    5;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGK--CS 56
              |:| ||||| |||  :  ||     |  ::  | ::|| |      |:|     ||  |
Db          1 MKILYLLFAFLFLAFLSEPG-----NAYKR--CHIKGGHCFPKGKICIPPSSDFGKMDCP 53

Qy         57 TRGRKCCRR 65
                | ||||::
Db         54 WR-RKCCKK 61


RESULT 10
BD05_BOVIN
ID   BD05_BOVIN     STANDARD;      PRT;    64 AA.
AC   P46163; O97533;
DT   01-NOV-1995 (Rel. 32, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-defensin 5 precursor (BNDB-5) (BNBD-5).
GN   DEFB5 OR BNBD5.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kurts B., Pitra C., Schwerin M., Seyfert H.-M.;
RT   "Beta defensin-encoding genes are selected for divergent sequences of
RT   the mature anti-bacterial peptide.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-54 FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Alveolar macrophage;
RX   MEDLINE=98114406; PubMed=9453661;
RA   Ryan L.K., Rhodes J., Bhat M., Diamond G.;
RT   "Expression of beta-defensin genes in bovine alveolar macrophages.";
RL   Infect. Immun. 66:878-881(1998).
RN   [3]
RP   SEQUENCE OF 23-64, FUNCTION, AND TISSUE SPECIFICITY.
RC   STRAIN=Hereford; TISSUE=Neutrophils;
RX   MEDLINE=93203264; PubMed=8454635;
RA   Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
RA   Smith W., Henschen A.H., Cullor J.S.;
RT   "Purification, primary structures, and antibacterial activities of
RT   beta-defensins, a new family of antimicrobial peptides from bovine
RT   neutrophils.";
RL   J. Biol. Chem. 268:6641-6648(1993).
RN   [4]
RP   REVISIONS TO C-TERMINUS.
RA   Selsted M.E.;
RL   Submitted (MAY-1996) to the SWISS-PROT data bank.
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY. ACTIVE AGAINST E.COLI ML35
CC       BUT NOT AGAINST S.AUREUS 502A.
CC   -!- TISSUE SPECIFICITY: NEUTROPHILIC GRANULES. ALVEOLAR MACROPHAGES.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AJ278799; CAC15400.1; -.
DR   EMBL; AF014108; AAD01523.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     22
FT   CHAIN        23     64       BETA-DEFENSIN 5.
FT   MOD_RES      23     23       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
```

```
FT   DISULFID     43     61       BY SIMILARITY.
FT   CONFLICT     54     54       F -> S (IN REF. 2).
SQ   SEQUENCE   64 AA;  7228 MW;  125A5278709131FC CRC64;

  Query Match             28.9%;  Score 106;  DB 1;  Length 64;
  Best Local Similarity   40.0%;  Pred. No. 1.3e-05;
  Matches   26;  Conservative    5;  Mismatches   32;  Indels    2;  Gaps    1;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||:|:||  |||| |    |   ::   |  ||   | |  :||     ||| |
Db          1 MRLHHLLLVLLFLVLSAGSGFTQVVRNPQS--CRWNMGVCIPISCPGNMRQIGTCFGPRV 58

Qy         61 KCCRR 65
              ||||
Db         59 PCCRR 63


RESULT 11
BD02_RAT
ID   BD02_RAT       STANDARD;      PRT;    63 AA.
AC   O88514;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-defensin 2 precursor (BD-2) (RBD-2).
GN   DEFB2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=99386883; PubMed=10456937;
RA   Jia H.P., Mills J.N., Barahmand-Pour F., Nishimura D.,
RA   Mallampali R.K., Wang G., Wiles K., Tack B.F., Bevins C.L.,
RA   McCray P.B. Jr.;
RT   "Molecular cloning and characterization of rat genes encoding
RT   homologues of human beta-defensins.";
RL   Infect. Immun. 67:4827-4833(1999).
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: Highly expressed in lung.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY. LAP/TAP
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF068861; AAC28072.1; -.
DR   HSSP; O15263; 1FD3.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL       1     20       POTENTIAL.
FT   PROPEP      21      ?       POTENTIAL.
FT   CHAIN       22     63       BETA-DEFENSIN 2.
FT   DISULFID    31     59       BY SIMILARITY.
FT   DISULFID    38     52       BY SIMILARITY.
FT   DISULFID    42     60       BY SIMILARITY.
SQ   SEQUENCE   63 AA;  6946 MW;  826099DE2144ACF4 CRC64;

  Query Match             27.4%;  Score 100.5;  DB 1;  Length 63;
  Best Local Similarity   37.9%;  Pred. No. 5.5e-05;
  Matches   25;  Conservative    7;  Mismatches   31;  Indels    3;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||: | : | |:      ||      | :|| |     |     ||| |
Db          1 MRIHYLLFSFLLVLLSPLSAFTQSIN--NPITCLTKGGVCWG-PCTGGFRQIGTCGLPRV 57

Qy         61 KCCRRK 66
              :||::|
Db         58 RCCKKK 63


RESULT 12
BD01_CAPHI
ID   BD01_CAPHI     STANDARD;      PRT;    64 AA.
AC   O97946;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Beta-defensin 1 precursor (BD-1).
GN   DEFB1.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tongue;
RA   Zhao C., Nguyen T., Lehrer R.I.;
RT   "Molecular cloning and tissue expression of goat b-defensin-1.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y17679; CAA76811.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL       1     20       POTENTIAL.
FT   PROPEP      21     26       POTENTIAL.
FT   CHAIN       27     64       BETA-DEFENSIN 1.
FT   DISULFID    31     60       BY SIMILARITY.
FT   DISULFID    38     53       BY SIMILARITY.
FT   DISULFID    43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7258 MW;  492B824C8F57B042 CRC64;

  Query Match             27.2%;  Score 100;  DB 1;  Length 64;
  Best Local Similarity   37.9%;  Pred. No. 6.4e-05;
  Matches   25;  Conservative    5;  Mismatches   34;  Indels    2;  Gaps    1;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||:|:||  | || |    | |       :  |    | ||:  |     ||| |
Db          1 MRLHHLLLVLFPLVL--SAGSGFTQGIRSRRSCHRNKGVCALTRCPRNMRQIGTCFGPPV 58

Qy         61 KCCRRK 66
              ||||:|
Db         59 KCCRKK 64


RESULT 13
BD02_SHEEP
ID   BD02_SHEEP     STANDARD;      PRT;    64 AA.
AC   O19039;
```

```
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Beta-defensin 2 precursor (BD-2) (sBD2).
GN   DEFB2 OR BD2.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98138497; PubMed=9478010;
RA   Huttner K.M., Brezinski-Caliguri D.J., Mahoney M.M., Diamond G.;
RT   "Antimicrobial peptide expression is developmentally regulated in the
RT   ovine gastrointestinal tract.";
RL   J. Nutr. 128:297S-299S(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RX   MEDLINE=98121317; PubMed=9461419;
RA   Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT   "Localization and genomic organization of sheep antimicrobial peptides
RT   genes.";
RL   Gene 206:85-91(1998).
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U75251; AAB61996.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23     64       BETA-DEFENSIN 2.
FT   DISULFID    31     60       BY SIMILARITY.
FT   DISULFID    38     53       BY SIMILARITY.
FT   DISULFID    43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7078 MW;  C744942B364716C0 CRC64;

  Query Match             26.7%;  Score 98;  DB 1;  Length 64;
  Best Local Similarity   37.3%;  Pred. No. 0.00011;
  Matches   25;  Conservative    8;  Mismatches   30;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGH-GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||:|:||  | |: |    |   |: ::|    || : | | :  |     ||| |
Db          1 MRLHHLLLLVLPFVVLSAGSGFTHGVTDSLS---CRWKKGICVLTRCPGTMRQIGTCFGPP 57

Qy         60 RKCCRRK 66
               |||| |
Db         58 VKCCRLK 64


RESULT 14
BDC7_BOVIN
ID   BDC7_BOVIN     STANDARD;      PRT;    53 AA.
AC   O18815;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Beta-defensin C7 precursor (BBD(C7)) (Fragment).
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Small intestine;
RX   MEDLINE=98147718; PubMed=9488394;
RA   Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA   Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA   Wines M., Hwang S., Bevins C.L.;
RT   "Enteric beta-defensin: molecular cloning and characterization of a
RT   gene with inducible intestinal epithelial cell expression associated
RT   with Cryptosporidium parvum infection.";
RL   Infect. Immun. 66:1045-1056(1998).
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF016395; AAC48802.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   NON_TER      1      1
FT   SIGNAL      <1      ?       POTENTIAL.
FT   PROPEP       ?     15       POTENTIAL.
FT   CHAIN       16     53       BETA-DEFENSIN C7.
FT   DISULFID    20     49       BY SIMILARITY.
FT   DISULFID    27     42       BY SIMILARITY.
FT   DISULFID    32     50       BY SIMILARITY.
SQ   SEQUENCE   53 AA;  5650 MW;  34659DF3A0489F4A CRC64;

  Query Match             25.6%;  Score 94;  DB 1;  Length 53;
  Best Local Similarity   41.1%;  Pred. No. 0.00026;
  Matches   23;  Conservative    5;  Mismatches   22;  Indels    6;  Gaps    1;

Qy          9 ALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCR 64
              |||||  |     |  | ::      || :|| | :: |     ||| |  | ||||
Db          2 ALLFLVLSAGSGISGPLS------CRRKGGICILIRCPGPMRQIGTCFGRPVKCCR 51


RESULT 15
BD01_SHEEP
ID   BD01_SHEEP     STANDARD;      PRT;    64 AA.
AC   O19038;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-defensin 1 precursor (BD-1) (sBD1).
GN   DEFB1.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98138497; PubMed=9478010;
RA   Huttner K.M., Brezinski-Caliguri D.J., Mahoney M.M., Diamond G.;
RT   "Antimicrobial peptide expression is developmentally regulated in the
RT   ovine gastrointestinal tract.";
RL   J. Nutr. 128:297S-299S(1998).
```

```
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RX   MEDLINE=98121317; PubMed=9461419;
RA   Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT   "Localization and genomic organization of sheep antimicrobial peptides
RT   genes.";
RL   Gene 206:85-91(1998).
CC   -!- FUNCTION: HAS BACTERICIDAL ACTIVITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U75250; AAB61995.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23     64       BETA-DEFENSIN 1.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7244 MW;  3529A9B76ABD023A CRC64;

  Query Match           25.3%;  Score 93;  DB 1;  Length 64;
  Best Local Similarity 37.3%;  Pred. No. 0.0004;
  Matches   25;  Conservative    5;  Mismatches   33;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGH-GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||:|:||  | |: |    |   |: | |    |    | |    |     ||| |
Db          1 MRLHHLLLVLFFVVLSAGSGFTQGVRNRLS---CHRNKGVCVPSRCPRHMRQIGTCRGPP 57

Qy         60 RKCCRRK 66
               ||||:|
Db         58 VKCCRKK 64


Search completed: October 31, 2003, 14:02:00
Job time : 24 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 31, 2003, 13:59:07 ; Search time 95 Seconds
(without alignments)
181.995 Million cell updates/sec

Title: US-09-872-852-2
Perfect score: 367
Sequence: 1 MRIHYLLFALLFLFLVPVPG.....KEEQIGKCSTRGRKCCRRKK 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	355	96.7	67	4	Q8NFG6	Q8nfg6 homo sapien
2	349	95.1	64	6	Q95JD2	Q95jd2 pan troglod
3	135	36.8	64	6	Q9TT12	Q9tt12 pan troglod
4	134	36.5	64	6	Q9BDS9	Q9bds9 macaca mula
5	105	28.6	64	6	O97942	O97942 capra hircu
6	105	28.6	65	13	Q9PWF3	Q9pwf3 crotalus du
7	103	28.1	65	13	O57540	O57540 crotalus du
8	102	27.8	71	11	Q91V70	Q91v70 mus musculu
9	99	27.0	64	11	Q9EPV9	Q9epv9 mus musculu
10	98.5	26.8	63	11	Q91VD6	Q91vd6 mus musculu
11	96.5	26.3	80	13	Q9DG58	Q9dg58 gallus gall
12	96	26.2	64	13	O73799	O73799 crotalus du
13	93	25.3	60	11	Q8R556	Q8r556 mus musculu
14	92	25.1	60	11	Q91V82	Q91v82 mus musculu
15	89.5	24.4	59	13	Q9DG57	Q9dg57 meleagris g
16	82.5	22.5	64	11	Q8R2I4	Q8r2i4 mus musculu
17	79.5	21.7	67	11	Q8R2I6	Q8r2i6 mus musculu
18	78	21.3	80	6	Q9MZ26	Q9mz26 pan troglod
19	76	20.7	80	4	Q9H4P9	Q9h4p9 homo sapien
20	75	20.4	68	6	Q95M68	Q95m68 gorilla gor
21	74.5	20.3	79	11	Q8R2I5	Q8r2i5 mus musculu
22	74	20.2	69	11	Q8K4N2	Q8k4n2 mus musculu
23	73.5	20.0	65	13	Q9DG59	Q9dg59 gallus gall
24	73	19.9	68	6	Q95M69	Q95m69 pan troglod
25	70	19.1	80	6	Q8SQD3	Q8sqd3 macaca mula
26	70	19.1	82	6	Q8SQC5	Q8sqc5 macaca mula
27	68.5	18.7	39	4	Q8NES9	Q8nes9 homo sapien
28	68	18.5	68	6	Q95M66	Q95m66 saguinus oe
29	67	18.3	68	6	Q95M67	Q95m67 cercopithec
30	67	18.3	68	6	Q95J22	Q95j22 hylobates m
31	66.5	18.1	63	11	Q8R2I3	Q8r2i3 mus musculu
32	66	18.0	68	6	Q95J24	Q95j24 cercopithec
33	66	18.0	68	11	Q8VBV2	Q8vbv2 rattus norv
34	66	18.0	919	13	Q8UVR0	Q8uvr0 gallus gall
35	66	18.0	936	13	Q8UVQ9	Q8uvq9 gallus gall
36	64.5	17.6	77	11	Q8R2I7	Q8r2i7 mus musculu
37	64	17.4	68	6	Q95J18	Q95j18 presbytis m
38	64	17.4	624	13	Q9DEQ0	Q9deq0 oncorhynchu
39	63.5	17.3	1593	13	Q8JHV8	Q8jhv8 brachydanio
40	63	17.2	329	4	Q96S04	Q96s04 homo sapien
41	62.5	17.0	565	2	Q9F3S8	Q9f3s8 rhodothermu
42	62	16.9	50	6	Q8WNZ3	Q8wnz3 natalus str
43	62	16.9	4578	13	O42181	O42181 fugu rubrip
44	61.5	16.8	77	4	Q8IZN8	Q8izn8 homo sapien
45	61.5	16.8	78	4	Q8NG35	Q8ng35 homo sapien

ALIGNMENTS

RESULT 1
Q8NFG6
ID Q8NFG6 PRELIMINARY; PRT; 67 AA.
AC Q8NFG6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-defensin-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tonsil;
RA Chen S., He F., Li R.;
RT "Cloning and expression of Chinese human beta defensin-3.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF516673; AAM62424.1; -.
SQ SEQUENCE 67 AA; 7750 MW; 15266DE1C90D5709 CRC64;

Query Match 96.7%; Score 355; DB 4; Length 67;
Best Local Similarity 98.5%; Pred. No. 4.9e-38;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSRLPKEEQIGKCSTRGR 60

Qy         61 KCCRRKK 67
              |||||||
Db         61 KCCRRKK 67
```

RESULT 2
Q95JD2
ID Q95JD2 PRELIMINARY; PRT; 64 AA.
AC Q95JD2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Beta-defensin-3 (Fragment).
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Duits L.A., Langermans J.A.M., Ravensbergen B., Paltansing S.,
RA   Vervenne R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT   "Expression of chimpanzee (Pan troglodytes) beta-defensin-3.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY033883; AAK61549.1; -.
DR   InterPro; IPR001855; Defensin_beta.
DR   Pfam; PF00711; Defensin_beta; 1.
FT   NON_TER      64     64
SQ   SEQUENCE   64 AA;  7299 MW;  01C90D4B60218DC8 CRC64;

  Query Match             95.1%;  Score 349;  DB 6;  Length 64;
  Best Local Similarity   98.4%;  Pred. No. 2.7e-37;
  Matches   63;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              |||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLTCLPKEEQIGKCSTRGR 60

Qy         61 KCCR 64
              ||||
Db         61 KCCR 64


RESULT 3
Q9TT12
ID   Q9TT12      PRELIMINARY;      PRT;    64 AA.
AC   Q9TT12;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-defensin-2.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Duits L.A., Langermans J.A.M., van der Straaten T., Vervenne R.A.W.,
RA   Paltansing S., Frost P.A., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT   "Expression of beta-defensin-2 in chimpanzee (Pan troglodytes).";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF209855; AAF20154.1; -.
DR   HSSP; O15263; 1FD3.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
SQ   SEQUENCE   64 AA;  7068 MW;  B0D2454CE7ACCD13 CRC64;

  Query Match             36.8%;  Score 135;  DB 6;  Length 64;
  Best Local Similarity   42.4%;  Pred. No. 8.2e-10;
  Matches   28;  Conservative   12;  Mismatches   22;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPG-HGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||: |||| ||:||:|:||  ||| : :    |  |  |  : |  : :||| |   |
Db          1 MRVLYLLFSFLFIFLMPLPGVFGGISDPVT---CLKSGAICHPVFCPRRYKQIGTCGLPG 57

Qy         60 RKCCRR 65
              |||::
Db         58 TKCCKK 63


RESULT 4
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Q9BDS9
ID   Q9BDS9      PRELIMINARY;      PRT;    64 AA.
AC   Q9BDS9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-defensin 2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21137962; PubMed=11238224;
RA   Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
RT   "Rhesus Monkey (Macaca mulatta) Mucosal Antimicrobial Peptides Are
RT   Close Homologues of Human Molecules.";
RL   Clin. Diagn. Lab. Immunol. 8:370-375(2001).
DR   EMBL; AF288286; AAK26259.1; -.
DR   HSSP; O15263; 1FD3.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
SQ   SEQUENCE   64 AA;  7065 MW;  BB26454CE7ACCDDF CRC64;

  Query Match             36.5%;  Score 134;  DB 6;  Length 64;
  Best Local Similarity   42.4%;  Pred. No. 1.1e-09;
  Matches   28;  Conservative   12;  Mismatches   22;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPG-HGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||: |||| ||:||:|:||  ||| : :    |  |  |  : |  : :||| |   |
Db          1 MRVLYLLFSFLFIFLMPLPGVFGGIGDPVT---CLKNGAICHPVFCPRRYKQIGTCGLPG 57

Qy         60 RKCCRR 65
              |||::
Db         58 TKCCKK 63


RESULT 5
O97942
ID   O97942      PRELIMINARY;      PRT;    64 AA.
AC   O97942;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Beta defensin-2 precursor.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002622; PubMed=10531296;
RA   Zhao C., Nguyen T., Liu L., Shamova O., Brogden K., Lehrer R.I.;
RT   "Differential expression of caprine beta-defensins in digestive and
RT   respiratory tissues.";
RL   Infect. Immun. 67:6221-6224(1999).
DR   EMBL; AJ009877; CAA08905.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Signal.
FT   SIGNAL       1     26       POTENTIAL.
FT   CHAIN       27     64       BETA DEFENSIN-2.
SQ   SEQUENCE   64 AA;  7165 MW;  8672F55D9BF800BA CRC64;

  Query Match             28.6%;  Score 105;  DB 6;  Length 64;
  Best Local Similarity   43.3%;  Pred. No. 5.9e-06;
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  Matches   29;  Conservative    3;  Mismatches   31;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGH-GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              ||:|:|| || || |    |   ||||      |    | ||   |     ||| |
Db          1 MRLHHLLLALFFLVLSAGSGFTQGIINHRS---CYRNKGVCAPARCPRNMRQIGTCHGPP 57

Qy         60 RKCCRRK 66
                ||||:|
Db         58 VKCCRKK 64


RESULT 6
Q9PWF3
ID   Q9PWF3      PRELIMINARY;      PRT;    65 AA.
AC   Q9PWF3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Crotamine isoform precursor.
GN   CRO2 OR CRT-P1.
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99314847; PubMed=10484745;
RA   Radis-Baptista G., Oguiura N., Hayashi M.A.F., Camargo M.E., Grego K.,
RA   Brandt E.P., Yamane T.;
RT   "Nucleotide sequence of crotamine isoform precursors from a single
RT   South American rattlesnake (Crotalus durissus terrificus).";
RL   Toxicon 37:973-984(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=9706, and 9705; TISSUE=Liver;
RA   Radis-Baptista G., Oguiura N., Penteado-Rodrigues J., Yamane T.;
RT   "Structural organization of crotamine genes encoding a myotoxin in the
RT   venom of South American rattlesnake (Crotalus durissus terrificus).";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF053075; AAC06241.1; -.
DR   EMBL; AF223947; AAF34911.1; -.
DR   EMBL; AF223946; AAF34910.1; -.
DR   InterPro; IPR000881; Myotoxin.
DR   Pfam; PF00819; Myotoxins; 1.
DR   PRINTS; PR00283; MYOTOXIN.
DR   ProDom; PD005972; Myotoxin; 1.
DR   PROSITE; PS00459; MYOTOXINS; 1.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23     65       POTENTIAL.
SQ   SEQUENCE   65 AA;  7519 MW;  FD109153C5BCCE33 CRC64;

  Query Match             28.6%;  Score 105;  DB 13;  Length 65;
  Best Local Similarity   39.7%;  Pred. No. 5.9e-06;
  Matches   27;  Conservative    7;  Mismatches   24;  Indels   10;  Gaps    4;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGKCSTR 58
              |:| ||||| |||  :  ||     |  ::  |  :|| |      |||     ||   |
Db          1 MKILYLLFAFLFLAFLSEPG-----NAYKQ--CHKKGGHCFPKEKICLPPSSDFGKMDCR 53

Qy         59 GR-KCCRR 65
                | |||::
Db         54 WRWKCCKK 61


RESULT 7
O57540
ID   O57540      PRELIMINARY;      PRT;    65 AA.
AC   O57540;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Crotamine precursor.
GN   CRO1.
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99314847; PubMed=10484745;
RA   Radis-Baptista G., Oguiura N., Hayashi M.A., Camargo M.E., Grego K.F.,
RA   Oliveira E.B., Yamane T.;
RT   "Nucleotide sequence of crotamine isoform precursors from a single
RT   South American rattlesnake (Crotalus durissus terrificus).";
RL   Toxicon 37:973-984(1999).
DR   EMBL; AF044674; AAC02995.1; -.
DR   InterPro; IPR000881; Myotoxin.
DR   Pfam; PF00819; Myotoxins; 1.
DR   PRINTS; PR00283; MYOTOXIN.
DR   ProDom; PD005972; Myotoxin; 1.
DR   PROSITE; PS00459; MYOTOXINS; 1.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23     65       CROTAMINE.
SQ   SEQUENCE   65 AA;  7519 MW;  F840C453C5BCCE33 CRC64;

  Query Match             28.1%;  Score 103;  DB 13;  Length 65;
  Best Local Similarity   38.2%;  Pred. No. 1.1e-05;
  Matches   26;  Conservative    8;  Mismatches   24;  Indels   10;  Gaps    4;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGKCSTR 58
              |:| ||||| |||  :  ||     |  ::  |  :|| |      |:|     ||   |
Db          1 MKILYLLFAFLFLAFLSEPG-----NAYKQ--CHKKGGHCFPKEKICIPPSSDFGKMDCR 53

Qy         59 GR-KCCRR 65
                | |||::
Db         54 WRWKCCKK 61


RESULT 8
Q91V70
ID   Q91V70      PRELIMINARY;      PRT;    71 AA.
AC   Q91V70;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-defensin 7 precursor.
GN   DEFB7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Krause A.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Conejo-Garcia J.R., Nehls M.C., Wattler S., Bals R., Heitland A.,
RA   Kluever E., Liepke C., Adermann K., Forssmann W.G.;
RT   "Cloning and characterization of mBD-7 and mBD-8, two novel mouse
RT   beta-defensins.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ298147; CAC44541.1; -.
DR   EMBL; AJ298148; CAC44542.1; -.
DR   MGD; MGI:2179200; Defb7.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
SQ   SEQUENCE   71 AA;  8292 MW;  8FB7A8A89146DF60 CRC64;
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  Query Match             27.8%;  Score 102;  DB 11;  Length 71;
  Best Local Similarity   40.6%;  Pred. No. 1.6e-05;
  Matches   26;  Conservative    8;  Mismatches   26;  Indels    4;  Gaps    3;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              |||||:|||  | : | |        ||:  |  |   || | :  |:    :|| |: |
Db          1 MRIHYVLFAFLLVLLSPFAAFSQDINS--KRACYREGGEC-LQRCIGLFHKIGTCNFR-F 56

Qy         61 KCCR 64
              |||:
Db         57 KCCK 60


RESULT 9
Q9EPV9
ID   Q9EPV9      PRELIMINARY;      PRT;    64 AA.
AC   Q9EPV9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Defensin beta 5.
GN   DEFB5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Adler D.A., Holloway J.L., Haldeman B.E., Rixon M., Jaspers S.,
RA   Fox B., Gosink J., Sheppard P., Presnell S., Gao Z., Whitmore T.,
RA   Stamm M., Laube D., Diamond G.;
RT   "EST and Genomic Database Mining Yield Novel Human and Mouse Beta-
RT   Defensins.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF318068; AAG49340.1; -.
DR   MGD; MGI:1933153; Defb5.
SQ   SEQUENCE   64 AA;  7087 MW;  6105153157A27B3B CRC64;

  Query Match             27.0%;  Score 99;  DB 11;  Length 64;
  Best Local Similarity   40.3%;  Pred. No. 3.5e-05;
  Matches   27;  Conservative    4;  Mismatches   32;  Indels    4;  Gaps    3;

Qy          1 MRIHYLLFALLFLFLVPVPG-HGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRG 59
              |||||||||  | : | |:       ||      | : || |  | |   | | |
Db          1 MRIHYLLFAFLLVLLCPLASDFSKTIN--NPVSCCMIGGICRYL-CKGNILQNGNCGVTS 57

Qy         60 RKCCRRK 66
                ||:||
Db         58 LNCCKRK 64


RESULT 10
Q91VD6
ID   Q91VD6      PRELIMINARY;      PRT;    63 AA.
AC   Q91VD6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-defensin 6.
GN   DEFB6 OR MBD-6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yamaguchi Y., Fukuhara S., Nagase T., Tomita T., Hitomi S., Kimura S.,
RA   Kurihara H., Ouchi Y.;
RT   "A novel mouse beta-defensin, mBD-6, predominantly expressed in
RT   skeletal muscle.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB063110; BAB61109.1; -.
DR   EMBL; AB063109; BAB61108.1; -.
DR   MGD; MGI:2151044; Defb6.
SQ   SEQUENCE   63 AA;  6977 MW;  15FDAB06429D924E CRC64;

  Query Match             26.8%;  Score 98.5;  DB 11;  Length 63;
  Best Local Similarity   37.9%;  Pred. No. 3.9e-05;
  Matches   25;  Conservative    7;  Mismatches   31;  Indels    3;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              |:|||||| : : | |:     :||:     |   || |   ||       | |
Db          1 MKIHYLLFAFILVMLSPLAAFSQLINS--PVTCMSYGGSCQ-RSCNGGFRLGGHCGHPKI 57

Qy         61 KCCRRK 66
              :|||||
Db         58 RCCRRK 63


RESULT 11
Q9DG58
ID   Q9DG58      PRELIMINARY;      PRT;    80 AA.
AC   Q9DG58;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Beta-defensin prepropeptide.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RX   MEDLINE=21153640; PubMed=11254635;
RA   Zhao C., Nguyen T., Liu L., Sacco R.E., Brogden K.A., Lehrer R.I.;
RT   "Gallinacin-3, an Inducible Epithelial beta-Defensin in the Chicken.";
RL   Infect. Immun. 69:2684-2691(2001).
DR   EMBL; AF181952; AAG09212.1; -.
DR   InterPro; IPR006080; Defensin_mammal.
DR   SMART; SM00048; DEFSN; 1.
SQ   SEQUENCE   80 AA;  8746 MW;  496BBC6BFB3F5C3F CRC64;

  Query Match             26.3%;  Score 96.5;  DB 13;  Length 80;
  Best Local Similarity   41.5%;  Pred. No. 9e-05;
  Matches   27;  Conservative    2;  Mismatches   27;  Indels    9;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              |||  |||      |||     |             ||:||| | | ||      ||||:|
Db          1 MRIVYLLIPFFLLFLQGAAG--------TATQCRIRGGFCRVGSCRFPHIAIGKCAT-FI 51

Qy         61 KCCRR 65
                || |
Db         52 SCCGR 56


RESULT 12
O73799
ID   O73799      PRELIMINARY;      PRT;    64 AA.
AC   O73799;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Crotamine.
GN   CRO3.
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99314847; PubMed=10484745;
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RA   Radis-Baptista G., Oguiura N., Hayashi M.A., Camargo M.E., Grego K.F.,
RA   Oliveira E.B., Yamane T.;
RT   "Nucleotide sequence of crotamine isoform precursors from a single
RT   South American rattlesnake (Crotalus durissus terrificus).";
RL   Toxicon 37:973-984(1999).
DR   EMBL; AF055988; AAC19036.1; -.
DR   InterPro; IPR000881; Myotoxin.
DR   Pfam; PF00819; Myotoxins; 1.
DR   PRINTS; PR00283; MYOTOXIN.
DR   ProDom; PD005972; Myotoxin; 1.
DR   PROSITE; PS00459; MYOTOXINS; 1.
SQ   SEQUENCE   64 AA;  7391 MW;  9B763190F34CCE35 CRC64;

  Query Match             26.2%;  Score 96;  DB 13;  Length 64;
  Best Local Similarity   37.9%;  Pred. No. 8.4e-05;
  Matches   25;  Conservative    7;  Mismatches   24;  Indels   10;  Gaps    4;

Qy          3 IHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLS--CLPKEEQIGKCSTRGR 60
              | ||||| |||  :  ||     |  ::  |  :|| |      |:|     ||   | |
Db          2 ILYLLFAFLFLAFLSEPG-----NAYKQ--CHKKGGHCFPKEKICIPPSSDFGKMDCRWR 54

Qy         61 -KCCRR 65
               |||::
Db         55 WKCCKK 60


RESULT 13
Q8R556
ID   Q8R556      PRELIMINARY;      PRT;    60 AA.
AC   Q8R556;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Defensin related peptide.
GN   DEFR1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57Bl/6J;
RA   Morrison G.M.;
RT   "Identification and characterisation of Defr1 : a novel murine beta
RT   defensin related gene.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ344114; CAC86998.1; -.
DR   InterPro; IPR001855; Defensin_beta.
DR   Pfam; PF00711; Defensin_beta; 1.
SQ   SEQUENCE   60 AA;  6820 MW;  3702A95649120351 CRC64;

  Query Match             25.3%;  Score 93;  DB 11;  Length 60;
  Best Local Similarity   35.9%;  Pred. No. 0.00019;
  Matches   23;  Conservative    7;  Mismatches   30;  Indels    4;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||  | : | |:      ||    |   :| |     |:    :|| | :
Db          1 MRIHYLLFTFLLVLLSPLAAFSQKINDPVTY---IRNGGICQYRCIGLRHKIGTCGS-PF 56

Qy         61 KCCR 64
              |||:
Db         57 KCCK 60


RESULT 14
Q91V82
ID   Q91V82      PRELIMINARY;      PRT;    60 AA.
AC   Q91V82;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Beta-defensin 8 (Beta-defensin 6).
GN   DEFB8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Conejo-Garcia J.R., Nehls M.C., Wattler S., Bals R., Heitland A.,
RA   Kluever E., Liepke C., Adermann K., Forssmann W.G.;
RT   "Cloning and characterization of mBD-7 and mBD-8, two novel mouse
RT   beta-defensins.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Krause A.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ300674; CAC44635.1; -.
DR   EMBL; AJ300673; CAC44634.1; -.
DR   InterPro; IPR001855; Defensin_beta.
DR   Pfam; PF00711; Defensin_beta; 1.
SQ   SEQUENCE   60 AA;  6760 MW;  7213024CF909A59B CRC64;

  Query Match             25.1%;  Score 92;  DB 11;  Length 60;
  Best Local Similarity   37.5%;  Pred. No. 0.00026;
  Matches   24;  Conservative    7;  Mismatches   29;  Indels    4;  Gaps    3;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||||||||  | : | |:      ||  :   |   || |    |:    :|| | :
Db          1 MRIHYLLFTFLLVLLSPLAAFSQKIN--EPVSCIRNGGICQ-YRCIGLRHKIGTCGS-PF 56

Qy         61 KCCR 64
              |||:
Db         57 KCCK 60


RESULT 15
Q9DG57
ID   Q9DG57      PRELIMINARY;      PRT;    59 AA.
AC   Q9DG57;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Beta-defensin prepropeptide.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RX   MEDLINE=21153640; PubMed=11254635;
RA   Zhao C., Nguyen T., Liu L., Sacco R.E., Brogden K.A., Lehrer R.I.;
RT   "Gallinacin-3, an Inducible Epithelial beta-Defensin in the Chicken.";
RL   Infect. Immun. 69:2684-2691(2001).
DR   EMBL; AF181953; AAG09213.1; -.
SQ   SEQUENCE   59 AA;  6604 MW;  39F0CEEB91AE3E35 CRC64;

  Query Match             24.4%;  Score 89.5;  DB 13;  Length 59;
  Best Local Similarity   39.7%;  Pred. No. 0.00053;
  Matches   25;  Conservative    2;  Mismatches   27;  Indels    9;  Gaps    2;

Qy          1 MRIHYLLFALLFLFLVPVPGHGGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGR 60
              ||| ||||    |||    |            ||:||| |   ||      | ||:|
Db          1 MRIVYLLFPFFLLFLQSAAG--------TPIQCRIRGGFCRFGSCRFPHIAIAKCAT-FI 51

Qy         61 KCC 63
              ||
Db         52 PCC 54


Search completed: October 31, 2003, 14:03:44
Job time : 98 secs
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